

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 08:33:07 ; Search time 1398.42 Seconds
(without alignments)
11033.514 Million cell updates/sec

Title: US-09-727-855B-1

Perfect score: 3632

Sequence: 1 tctgttgataatcttctta.....aagagcttgacattgttag 3632

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002s.*

7: Geneseqn2003as.*

8: Geneseqn2003bs.*

9: Geneseqn2003cs.*

10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84.2	2.3	728	2 AAT85876	Aat85876 Malassezia
2	78.8	2.2	897	9 ADD35245	Add35245 Mouse mlt
3	74	2.0	270	7 AAT33645	Abt33645 Anticance
4	74	2.0	627	2 AAT70431	Aag70431 MHS:MnSOD
5	74	2.0	666	6 AAT09580	Abt09580 Phase-1 R
6	74	2.0	813	2 AAT053193	Aag53193 MnSOD cDN
7	74	2.0	813	2 AAT15589	Aat15589 Human man
8	74	2.0	813	2 AAT34277	Aat34277 Human man
9	74	2.0	813	2 AAT24998	Aax24998 Human nat
10	74	2.0	813	3 AAT63891	Aag63891 cDNA enco
11	74	2.0	849	6 AAT84891	Abn84891 Human man
12	74	2.0	849	6 ABA94453	Aba94453 Human man
13	74	2.0	930	9 ADE76309	Ade76309 Human BSK
14	74	2.0	972	7 ABX63836	Abx63836 Human cDN
15	74	2.0	1026	6 ABX6512	Abx6512 Lung canc
16	74	2.0	1026	6 ABK84524	Abk84524 Human cDN
17	74	2.0	1046	3 AAT094284	Aag94284 Human man
18	74	2.0	1438	3 AAT75734	Aa75734 Nucleotid
19	74	2.0	1492	6 ABK63720	Abk63720 Rat seque
20	74	2.0	1492	9 ADB58236	Adb58236 Toxicity-
21	74	2.0	2504	4 AAL26545	Aal26545 Human bre
22	73	2.0	325	6 AAD39690	Aad39690 Human Mns
23	73	2.0	414	3 AAC02178	Aac02178 Human sec

24	72.6	2.0	424	7 ABX49579	Abx49579 Bovine ES
25	72.4	2.0	594	3 AAZ39779	Aaz39779 Human man
26	72.4	2.0	609	2 AAZ20194	Aaz20194 Mn-SOD (I
27	72.4	2.0	627	2 AAZ70432	Aaz70432 MHS2:MnSO
28	72.4	2.0	681	3 AAZ39781	Aaz39781 Human man
29	72.4	2.0	813	1 AAN71370	Aan71370 Sequence
30	72.4	2.0	813	1 AAN81158	Aan81158 cDNA enco
31	72.4	2.0	969	2 AAT31018	Aat31018 Human man
32	72.4	2.0	976	2 AAZ67474	Aaz67474 Human man
33	72.4	2.0	976	2 AAX33940	Aax33940 Human HCM
34	72.4	2.0	976	2 AAX08429	Aax08429 Human man
35	72.4	2.0	976	7 ABZ83721	Abz83721 Toxicolog
36	72.4	2.0	3789	3 AAZ39782	Aaz39782 Plasmid p
37	71	2.0	2208	7 ABX63709	Abx63709 Human cDN
38	71	2.0	3300	2 AAV31822	Aav31822 Mutant As
39	71	2.0	3300	2 AAZ20707	Aaz20707 A. oryzae
40	71	2.0	3300	6 ABA93439	Aba93439 Mutant As
41	70.8	1.9	977	2 AAV73824	Aav73824 Human SOD
42	70.6	1.9	631	7 ABZ56304	Abz56304 Aspergill
43	70.6	1.9	702	3 AAF14076	Aaf14076 Aspergill
44	68.6	1.9	2809	9 ADB68898	Adb68898 C. neofo
45	68.2	1.9	894	9 ADE25718	Ade25718 Human cDN

ALIGNMENTS

RESULT 1
AAT85876

ID AAT85876 standard; cDNA to mRNA; 728 BP.

XX AC AAT85876;

XX DT 27-AUG-2003 (revised)

DT 23-FEB-1998 (first entry)

XX Malassezia fungus MF-3 antigenic protein encoding cDNA.

XX Malassezia; fungus; antigenic; human; IgE; immunoglobulin E; antibody;
KW allergy; antigen; ds.

XX Malassezia.

XX FH Key Location/Qualifiers

XX FT CDS 4..621

XX FT /*tag= a

XX FT /product= "MR-3_antigenic_protein"

XX WO9721817-A1.

XX PD 19-JUN-1997.

XX PF 10-DEC-1996; 96WO-JP003602.

XX PR 12-DEC-1995; 95JP-00346627.

XX PR 05-SEP-1996; 96JP-00257612.

XX PR 05-SEP-1996; 96JP-00257613.

XX (TAKI) TAKARA SHUZO CO LTD.

XX Takesako K, Okado T, Yagihara T, Kuroda M, Onishi Y, Kato I;

XX Akiyama K, Yaeueda H, Yamaguchi H;

XX WPI; 1997-332788/30.

XX P-PSDB; AAW29770.

XX Antigenic proteins from the fungus Malassezia - bind to IgG antibodies
present in patients with Malassezia allergies, useful for diagnosis,
treatment and prevention of such conditions.

XX Claim 53; Page 76-77; 162pp; Japanese.

XX The present sequence encodes a specifically claimed antigenic protein

XX WPI; 2003-210360/20.
XX
XX DNA array for measuring expression of a number of different target gene
PT fragments for measuring sensitivity of tumors to anticancer agents.
XX
XX PS Disclosure; Page 73; 83pp; Japanese.
XX
XX The invention relates to a novel DNA array for measuring sensitivity of a
CC tumour to an anticancer agent comprising at least thirteen different
CC target gene fragments selected from at least two types of gene including
CC genes for, enzymes associated with nucleic acid metabolism, gene repair,
CC factors associated with drug tolerance, and housekeeping genes. The array
CC is used for large-scale gene-expression profiling, especially for
CC assaying the sensitivity of tumours to anti-cancer agents. This
CC polynucleotide sequence represents a target gene fragment of the
CC invention
XX
XX Sequence 270 BP; 72 A; 86 C; 66 G; 46 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 74; DB 7; Length 270;
Best Local Similarity 67.5%; Pred. No. 3.2e-11;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1307 GCCTGGAGCCCTCCATCTCCAGGAGATCATGACCCCTTCCACACACCAAGCACCATCAG 1366
Db 54 GCCTGGAGCCCTCCATCTCCAGGAGATCATGACCCCTTCCACACACCAAGCACCATCAG 113
QY 1367 ACTTATGTTAAACGGCTCAACGCTGCGGAGGAGCTACTCGGCGGTGTGGCAAGGAG 1426
Db 114 GCCTAGTGAACACCTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 173
QY 1427 GATGTGCTTACCCAGGTTAAGCTTTCAGTCTGTAC 1460
Db 174 GATGTTACAGCCAGATAGCTCTTCAGCTGCAC 207
RESULT 4
AAQ70431
ID AAQ70431 standard; DNA; 627 BP.
XX
XX AC AAQ70431;
XX
XX 25-MAR-2003 (revised)
DT 28-FEB-1995 (first entry)
XX
XX MHS:MnSOD variant.
XX
XX Manganese superoxide dismutase; MnSOD; oxygen; cosmetic; mutation;
KW arthritis; variant; enzyme; isoelectric point; inflammation; cancer;
KW premature retinopathy; hypertension; diabetes; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 7..606
FT /*tag= a
FT misc_difference 406..408
FT /*tag= b
FT /*transl_except= pos:406..408, aa:Gly
XX
XX WO9414950-A1.
XX
XX 07-JUL-1994.
XX
XX 28-DEC-1993; 93WO-JP001917.
XX
XX 28-DEC-1992; 92JP-00359959.
XX
XX (SIIT-) SII TECHNORESEARCH INC.
XX
XX Kondo M, Katsuta K;
XX

DR WPI; 1994-234688/28.
DR P-PSDB; AAR60360.
XX
XX Human variant manganese super-oxide dismutase with aminoacid mutation in
PT non-essential regions - for treatment of arthritis, active oxygen related
PT disorders and for cosmetics.
XX
XX Example 3; Page 16-17; 34pp; Japanese.
XX
XX Human variant manganese superoxide dismutase (Mn-SOD) comprises an amino
CC acid substitution in a region which does not affect enzyme activity, of a
CC positively charged amino acid residue, which has the effect of raising
CC the isoelectric point of the peptide. These Mn-SOD variants are useful as
CC medical preps. for the treatment of human arthritis and diseases caused
CC by active oxygen, and as cosmetic preps. They are also useful for
CC treatment of inflammation, cancer, premature retinopathy, hypertension
CC and diabetes. Examples of variant Mn-SODs are given in AAQ70431-32.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 627 BP; 175 A; 152 C; 160 G; 140 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 74; DB 2; Length 627;
Best Local Similarity 67.5%; Pred. No. 5.6e-11;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1307 GCCTGGAGCCCTCCATCTCCAGGAGATCATGACCCCTTCCACACCAAGCACCATCAG 1366
Db 46 GCCTGGAGCCCTCCATCTCCAGGAGATCATGACCCCTTCCACACCAAGCACCATCAG 105
QY 1367 ACTTATGTTAAACGGCTCAACGCTGCGGAGGAGCTACTCGGCGGTGTGGCAAGGAG 1426
Db 106 GCCTAGCTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 165
QY 1427 GATGTGCTTACCCAGGTTAAGCTTTCAGTCTGTAC 1460
Db 166 GATGTTACAGCCAGATAGCTCTTCAGCTGCAC 199
RESULT 5
ABT09580
ID ABT09580 standard; DNA; 666 BP.
XX
XX AC ABT09580;
XX
XX 05-DEC-2002 (first entry)
DT
XX
XX Phase-1 Rat CT gene SEQ ID No 668.
DE
XX
XX Rat; toxicity study; rat toxic response gene; toxicological response;
KW drug development; phase-1 rat CT gene; ds.
XX
XX Rattus sp.
XX
XX WO200266682-A2.
XX
XX 29-AUG-2002.
XX
XX 29-JAN-2002; 2002WO-US002935.
XX
XX 29-JAN-2001; 2001US-0264933P.
PR 26-JUL-2001; 2001US-0308161P.
XX
XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX
XX Farris G, Hicken SH, Farr SB;
PI WPI; 2002-674961/72.
XX
XX Evaluating the toxicity of an agent, useful in drug development or in
PT determining toxicological responses to a new drug, by determining the
PT expression of rat toxicologically relevant genes in the test animal in
PT response to the test agent.
XX

PS Disclosure; Page 270; 388pp; English.

XX The invention relates to a method used for evaluating the toxicity of an

CC agent comprising determining the expression of a rat toxic response

CC gene(s) in the test animal in response to the agent. The method is useful

CC in drug development, particularly for conducting toxicity studies and

CC analysis before a new drug or compound is approved for human consumption

CC or use. The method is also useful in determining toxicological responses

CC to a new drug. This polynucleotide sequence represents a phase-1 rat CT

CC gene of the invention

XX

SQ Sequence 666 BP; 172 A; 164 C; 182 G; 146 T; 0 U; 2 Other;

Query Match 2.0%; Score 74; DB 6; Length 666;

Best Local Similarity 67.5%; Pred. No. 5.9e-11;

Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

OY 1307 GCCCTGGAGCCCTCCATCTCCAAAGGAGATCATGACCCCTTACCACCAAGCACCATCAG 1366

DB 124 CGCTGGAGCCGACATTAACGGCGAGATCATGCAGCTGCACCAAGCACCACGCG 183

OY 1367 ACTTATGTATACGGCTCAAGCTGCCGAGGAGAGCTACTGCGCGCTGTGGGCAAGGAG 1426

DB 184 ACCTACGTGAACAATCTGACGTCACCGAGGAGAGTACCAAGGCGCTGCCCAAGGGA 243

OY 1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460

DB 244 GATGTACAATCAGTTGCTTCTTACGCTGCAC 277

RESULT 6

AAQ53193

ID AAQ53193 standard; cDNA; 813 BP.

XX

AC AAQ53193;

XX

DT 25-MAR-2003 (revised)

DT 21-JUN-1994 (first entry)

XX

DE MnSOD cDNA.

XX

MnSOD; manganese superoxide dismutase; N-terminal; catalyst; reperfusion;

KW injury; ischaemia; superoxide; SO; molecular oxygen; anti-inflammatory;

KW ss.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT CDS 43..711

FT /*tag= a

FT /product= "MnSOD"

XX

US5270195-A.

XX

14-DEC-1993.

XX

10-JUL-1992; 92US-00912213.

XX

22-NOV-1985; 85US-00801090.

PR 12-SEP-1986; 86US-00907051.

PR 29-OCT-1986; 86IE-00002851.

PR 27-MAR-1987; 87US-00032734.

PR 13-DEC-1989; 89US-00453057.

XX

(BIOT-) BIO-TECHNOLOGY GENERAL CORP.

XX

Beck Y, Hartman JR;

XX

WPI; 1993-404931/50.

DR P-PSDB; AAR44801.

XX

Expression plasmid in Escherichia coli host system - encodes human

XX manganese superoxidizedismutase analogue, useful for e.g. treating

PT

inflammation.

XX

Claim 1; Fig 1a-1c; 27pp; English.

XX

The sequence encodes a manganese superoxide dismutase which can be used to

CC catalyse the reduction of superoxide (SO) radicals to hydrogen peroxide

CC and molecular oxygen. It can be used to reduce reperfusion injury

CC following ischaemia and prolong the survival of excised organs. It can

CC also be used as a long acting anti-inflammatory drug. (Updated on 25-MAR-

CC 2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)

XX

SQ Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;

Query Match 2.0%; Score 74; DB 2; Length 813;

Best Local Similarity 67.5%; Pred. No. 6.7e-11;

Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

OY 1307 GCCCTGGAGCCCTCCATCTCCAAAGGAGATCATGACCCCTTACCACCAAGCACCATCAG 1366

DB 151 GCCCTGGAACTCATCATCAACGGCGAGATCATGCAGCTGCACCAAGCACCACGCG 210

OY 1367 ACTTATGTATACGGCTCAAGCTGCCGAGGAGAGCTACTGCGCGCTGTGGGCAAGGAG 1426

DB 211 GCCTACGTGAACAATCTGACGTCACCGAGGAGAGTACCAAGGCGCTGCCCAAGGGA 270

OY 1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460

DB 271 GATGTACAGCCAGATAGCTCTTACGCTGCAC 304

RESULT 7

AAT15589

ID AAT15589 standard; cDNA; 813 BP.

XX

AC AAT15589;

XX

DT 25-MAR-2003 (revised)

DT 06-APR-1996 (first entry)

XX

DE Human manganese superoxide-dismutase cDNA.

XX

Human; manganese superoxide-dismutase; T-lymphocyte; probe; cDNA;

KW Escherichia coli; plasmid pMS8-4; N-terminal truncation; cloning;

KW aminopeptidase; antiinflammatory; oxygen free radical scavenger;

KW synovial inflammation; arthritis; lung fibrosis; ds.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT CDS 43..711

FT /*tag= a

FT /product= "Manganese superoxide-dismutase"

FT /note= "EC-1.15.1.1"

FT sig_peptide 43..114

FT /*tag= b

FT mat_peptide 115..708

FT /*tag= c

XX

EP691401-A1.

XX

10-JAN-1996.

XX

25-MAR-1988; 95EP-00106995.

XX

27-MAR-1987; 87US-00032734.

PR 26-FEB-1988; 88US-00161117.

XX

(BIOT-) BIO-TECHNOLOGY GENERAL CORP.

XX

Hartman JR, Beck Y, Nimrod A;

XX

WPI; 1996-059735/07.

DR P-PSDB; AAR90713.

XX New human manganese superoxide dismutase analogues - having a Lys and
PT opt. His residue absent from the N-terminus, useful for treating e.g.
PT synovial inflammation, arthritis or lung fibrosis.
XX Example 1; Fig 1; 45pp; English.
XX The sequence encodes a human manganese superoxide-dismutase (MnSOD), and
CC has been isolated from a human T-lymphocyte cDNA library in phage lambda-
CC gt10 in Escherichia coli, by screening with a 5'-probe (AAT15591) and a
CC 3'-probe (AAT15592). The sequence of the insert in plasmid pMS8-4
CC (obtained by subcloning in plasmid pBR322) is shown. The cDNA may be
CC expressed in e.g. E. coli for production of recombinant MnSOD. The MnSOD
CC product may be cleaved with Aeromonas proteolytica aminopeptidase to
CC produce an N-terminally truncated analogue with lysine and optionally
CC histidine residues removed. The MnSOD analogue may be used in therapy of
CC conditions associated with generation of oxygen free radicals,
CC particularly synovial inflammation, arthritis and lung fibrosis.
CC (claimed). (Updated on 25-MAR-2003 to correct PF field.)
XX Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 74; DB 2; Length 813;
Best Local Similarity 67.5%; Pred. No. 6.7e-11;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1307 GCCTGGAGCCCTCCATCTCCAGGAGATCATGACCCCTTCAACACACCAAGCACCATCAG 1366
Db 151 GCCTGGAGCCCTCACATCAACGCGCAGATCATGCTGCACACAGCAGCACCACCGCG 210
QY 1367 ACTATGTTAACGGCTCAACGCTGCCGAGGAGCTACTCGGCCGCTGTGGCAAGGAG 1426
Db 211 GCCTAGCTGAACAACCTGAACGTCACCGAGGAGAGTACCAGGAGGGTTGGCCNAGGGA 270
QY 1427 GATGTCCTTACCAGGTTAAGCTTCACTCTGCTGTAC 1460
Db 271 GATGTTACAGCCAGATAGCTCTTTCAGCCTGCAC 304
RESULT 8
AAT34277
ID AAT34277 standard; cDNA; 813 BP.
XX AAT34277;
AC
DT 25-MAR-2003 (revised)
DT 24-OCT-1996 (first entry)
XX Human manganese superoxide dismutase cDNA.
XX Manganese superoxide dismutase; MnSOD; reperfusion injury; ischaemia;
KW bronchial pulmonary dysplasia; inflammation; antiinflammatory; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
FH CDS 43..711
FT /*tag= a
FT sig_peptide 43..114
FT /*tag= b
FT mat_peptide 115..708
FT /*tag= c
XX US5540911-A.
XX 30-JUL-1996.
XX 09-JAN-1995; 95US-00370461.
XX 22-NOV-1985; 85US-00801090.
PR 12-SEP-1986; 86US-00907051.
PR 29-OCT-1986; 86IE-00002851.
PR 27-MAR-1987; 87US-00032734.

PR 13-DEC-1989; 89US-00453057.
PR 10-JUL-1992; 92US-00912213.
PR 14-SEP-1993; 93US-00120951.
XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
XX Hartman JR, Beck Y;
XX WPI; 1996-361912/36.
DR P-PSDB; AAW00018.
XX Use of recombinant human manganese superoxide dismutase - for treating
PT inflammation or bronchial pulmonary dysplasia, reducing reperfusion
PT injury or prolonging organ survival.
XX Claim 1; Fig 1A-1C; 27pp; English.
XX A cDNA clone (AAT34277) codes for human manganese superoxide dismutase
CC (MnSOD) (AAW00018), an enzyme that catalyses the reduction of superoxide
CC radicals to H2O2 and O2. It was isolated from a human T-cell library
CC cloned into vector gt10 using probes (see also AAT34283-84) based on
CC portions of mature MnSOD. The MnSOD gene was also identified (see also
CC AAT34278-82). The cDNA can be used for the prodn. of recombinant MnSOD
CC using e.g. Escherichia coli cells as hosts. The MnSOD is useful for
CC reducing reperfusion injury, treating inflammation or bronchial pulmonary
CC dysplasia and for prolonging survival of excised organs. (Updated on 25-
CC MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR
CC field.)
XX Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 74; DB 2; Length 813;
Best Local Similarity 67.5%; Pred. No. 6.7e-11;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1307 GCCTGGAGCCCTCCATCTCCAGGAGATCATGACCCCTTCAACACACCAAGCACCATCAG 1366
Db 151 GCCTGGAGCCCTCACATCAACGCGCAGATCATGCTGCACACAGCAGCACCACCGCG 210
QY 1367 ACTATGTTAACGGCTCAACGCTGCCGAGGAGCTACTCGGCCGCTGTGGCAAGGAG 1426
Db 211 GCCTAGCTGAACAACCTGAACGTCACCGAGGAGAGTACCAGGAGGGTTGGCCNAGGGA 270
QY 1427 GATGTCCTTACCAGGTTAAGCTTCACTCTGCTGTAC 1460
Db 271 GATGTTACAGCCAGATAGCTCTTTCAGCCTGCAC 304
RESULT 9
AAX24998
ID AAX24998 standard; cDNA; 813 BP.
XX AAX24998;
AC
DT 05-JUL-1999 (first entry)
XX Human native manganese superoxide dismutase cDNA.
XX Superoxide dismutase; MnSOD; SOD; human; protein engineering;
KW enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
KW inflammation; reperfusion injury; therapy; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FH CDS 43..711
FT /*tag= a
FT sig_peptide 43..114
FT /*tag= b
FT mat_peptide 115..708
FT /*tag= c
XX WO913088-A1.

[illegible]

```

XX OS Homo sapiens.
XX FH Key
XX FT misc_feature Location/Qualifiers
FT 1..8 /*tag= a
FT /note= "EcoRI linker used in cloning"
FT CDS 100..768 /*tag= b
FT 100..768 /*tag= b
FT /product= "hsODm"
FT sig_peptide 100..171
FT /tag= c
FT mat_peptide 172..765
FT /tag= d
FT misc_feature 842..849
FT /tag= e
FT /note= "EcoRI linker used in cloning"
XX US2002081287-A1.
XX 27-JUN-2002.
XX 11-JUN-2001; 2001US-00878589.
XX 14-OCT-1986; 86US-00918534.
XX (CHIR ) CHIRON CORP.
XX Hallelwell RA, Bell GI, Mullenbach GT;
XX WPI; 2002-626527/67.
XX P-PSDB; ABB79798.
XX Preparing recombinant human manganese superoxide dismutase, useful in the
XX treatment of osteoarthritis and rheumatoid arthritis.
XX Example 1; Fig 4; 16pp; English.
XX The present sequence is the nucleotide sequence of human manganese
XX superoxide dismutase (hsODm) cDNA. The cDNA was isolated from an adult
XX human kidney cDNA library in lambda-gt10 using the probes given in
XX CC A8N84889-90. The invention relates to methods for hsODm gene cloning and
XX expression in microorganisms, especially Escherichia coli or
XX CC Saccharomyces cerevisiae. The hsODm cDNA is inserted into a vector for
XX expression in the microbial host, preferably under conditions which allow
XX CC for processing to remove the N-terminal methionine. The expression
XX product is useful for treating a patient having inflammatory joint
XX CC disease (e.g. osteoarthritis or rheumatoid arthritis), or to minimise
XX CC post-ischaemic tissue damage resulting from disease or surgery
XX SQ Sequence 849 BP; 256 A; 197 C; 227 G; 169 T; 0 U; 0 Other;
Query Match 2.0%; Score 74; DB 6; Length 849;
Best Local Similarity 67.5%; Pred. No. 6.9e-11;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1307 GCCTGAGCCCTCCATCTCCAAAGGAGATCATGACCTTCACACACCAAGCACCATCAG 1366
Db 208 GCCTGAGACCTCACATCAACGGCGAGATCATGACGTGCACACAGCAGCACCAGCG 267
QY 1367 ACTTATGTGTTAAACGGCTCAACGGTCCGAGGAGAGTCTCTCGGCCGCTGTGGGCAAGGAG 1426
Db 268 GCCTAGTGAACACCTGAACGTCACCGAGAGAGTACACGAGGCGTTGGCCAGGGA 327
QY 1427 GATGTGCTTACCCAGGTTAAGCTTTCAGTCTGTAC 1460
Db 328 GATGTTACAGCCAGATAGCTCTTCAGCCTGCAC 361
RESULT 12
ABA94453
ID ABA94453 standard; cDNA; 849 BP.
XX

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```

AC ABA94453;
XX 09-APR-2002 (first entry)
XX Human manganese superoxide dismutase (hsODm) encoding cDNA.
XX DE Human manganese superoxide dismutase; antiinflammatory; antiarthritic;
XX KW antirheumatic; vasotropic; osteopathic; hsODm; human; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 100..768 /*tag= a
XX FT /product= "hsODm"
XX FT sig_peptide 100..171
XX FT /tag= b
XX FT mat_peptide 172..765
XX FT /tag= c
XX US6326003-B1.
XX 04-DEC-2001.
XX 14-OCT-1986; 86US-00918534.
XX 14-OCT-1986; 86US-00918534.
XX (CHIR ) CHIRON CORP.
XX Hallelwell RA, Bell GI, Mullenbach GT;
XX WPI; 2002-129495/17.
XX P-PSDB; ABB07330.
XX Treating inflammatory joint disease such as osteoarthritis, rheumatoid
XX arthritis and post ischemic tissue injury, comprises injecting human
XX manganese superoxide dismutase.
XX Example 2; Fig 4; 14pp; English.
XX The invention relates to a method of treating a patient with inflammatory
XX joint disease. The method involves intra-articularly injecting into the
XX afflicted joint a solution of human manganese superoxide dismutase
XX (hsODm). The treatment is used to treat an inflammatory joint disease,
XX particularly osteoarthritis or rheumatoid arthritis. The method can also
XX be used to treat post ischemic tissue injury. The present sequence
XX represents a cDNA encoding the hsODm
XX SQ Sequence 849 BP; 256 A; 197 C; 227 G; 169 T; 0 U; 0 Other;
Query Match 2.0%; Score 74; DB 6; Length 849;
Best Local Similarity 67.5%; Pred. No. 6.9e-11;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1307 GCCTGAGCCCTCCATCTCCAAAGGAGATCATGACCTTCACACACCAAGCACCATCAG 1366
Db 208 GCCTGAGACCTCACATCAACGGCGAGATCATGACGTGCACACAGCAGCACCAGCG 267
QY 1367 ACTTATGTGTTAAACGGCTCAACGGTCCGAGGAGAGTCTCTCGGCCGCTGTGGGCAAGGAG 1426
Db 268 GCCTAGTGAACACCTGAACGTCACCGAGAGAGTACACGAGGCGTTGGCCAGGGA 327
QY 1427 GATGTGCTTACCCAGGTTAAGCTTTCAGTCTGTAC 1460
Db 328 GATGTTACAGCCAGATAGCTCTTCAGCCTGCAC 361
RESULT 13
ADE76309
ID ADE76309 standard; DNA; 930 BP.
XX
XX ADE76309;

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XX 29-JAN-2004 (first entry)
XX Human BSK-1H13 complementary strand DNA.
XX monocyte; macrophage; gene expression profile; rheumatoid arthritis;
XX chronic inflammatory disease; bacteria-induced inflammation;
XX arteriosclerosis; tumour; organ; tissue transplant; sepsis;
XX molecular classification; human; BSK; ss.
XX Homo sapiens.
XX EPI1310567-A2.
XX 14-MAY-2003.
XX 02-OCT-2002; 2002EP-00090348.
XX 09-NOV-2001; 2001DE-01055600.
XX (OLIG-) OLIGENE GMBH.
XX Stuhlmueller B, Haeupl T;
XX WPI; 2003-443090/42.
XX Device for diagnosis, prognosis and monitoring therapy of e.g. rheumatoid
XX arthritis, comprises immobilized gene sequences from monocyte-macrophage
XX cells.
XX Claim 29; SEQ ID NO 121; 180pp; German.
XX The invention relates to a novel device for diagnosis, prognosis and
XX monitoring of therapy having, on its surface, sequences of some or all of
XX specified monocyte-macrophage genes and also of other genes or RNA
XX complementary to the specified genes. The device of the invention may be
XX used to determine gene expression profiles for measurement of monocyte or
XX macrophage activation or inflammation in blood or other tissues, as well
XX as for the diagnosis, prognosis and monitoring therapy in cases of
XX rheumatoid arthritis, chronic inflammatory disease, chronic bacteria-
XX induced inflammation, arteriosclerosis, tumours, organ or tissue
XX transplants and sepsis. The device provides information for molecular
XX classification and staging of disease, creation of a patient-specific
XX prognostic profile and suggestions about molecular pathogenesis or
XX therapeutic effects, thus facilitating the development of new therapeutic
XX strategies and pharmacological concepts. The current sequence is that of
XX the human BSK DNA of the invention.
XX Sequence 930 BP; 242 A; 208 C; 206 G; 245 T; 0 U; 29 Other;
XX
XX Query Match 2.0%; Score 74; DB 9; Length 930;
XX Best Local Similarity 67.5%; Pred. No. 7.4e-11;
XX Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
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XX 1307 GCCTGGAGCCCTCCATCTCCAAAGGAGATCATGACCCCTTCCACCACCAAGCACCATCAG 1366
XX 67 GCCTGGAGCCCTCCATCAACCGCGAGATCATGCGAGTGCACACAGCAAGCACCACGGC 126
XX 1367 ACTATGTTAAGGCTCAAGCTCCGAGGAGACTACTCGGCGCTGTGGCAAGGAG 1426
XX 127 GCCTAGTGAACAACCTGAACCTACCGGAGGAGAGTACGAGGCGGTGGCCCAAGGA 186
XX 1427 GATGTCCTTACCAGGTAAAGCTTCAGTCTGTAC 1460
XX 187 GATGTTACGCCAGATAGTCTTTCAGCTGCAC 220
XX
XX RESULT 14
XX ABX63836
XX ID ABX63836 standard; cDNA; 972 BP.
XX AC ABX63836;
XX XX

DT 26-FEB-2003 (first entry)
XX Human cDNA #836 differentially expressed in activated vascular tissue.
XX Human; gene; ss; vascular tissue; cytostatic; atherosclerosis; cardiant;
XX hypotensive; antidiabetic; gynaecological; vasotropic; cerebroprotective;
XX gene therapy; vascular disease; cancer; coronary; artery disease;
XX hypertension; diabetes; pre-eclampsia; restenosis;
XX ischaemia-reperfusion injury; stroke.
XX Homo sapiens.
XX US2002137081-A1.
XX 26-SEP-2002.
XX 08-JAN-2002; 2002US-00044090.
XX 28-JUL-2000; 2000US-0222469P.
XX 08-JAN-2001; 2001US-0260483P.
XX (BAND/) BANDMAN O.
XX Bandman O;
XX WPI; 2003-110597/10.
XX Combination for diagnosing, staging, treating, or monitoring the
XX progression of treatment of a vascular disease, e.g. atherosclerosis,
XX comprises several cDNAs that are differentially expressed in activated
XX vascular tissue.
XX Claim 1; Page; 18pp; English.
XX This invention relates to a combination comprising several cDNAs that are
XX differentially expressed in activated vascular tissue. The invention also
XX discloses a high throughput method for detecting differentially expressed
XX cDNAs in a sample. The cDNAs of the invention may have
XX antiarteriosclerotic; cytostatic; cardiant; hypotensive; antidiabetic;
XX gynaecological; vasotropic and cerebroprotective activities and may be
XX used in gene therapy. The cDNAs of the invention may be used in a high-
XX throughput methods for detecting differential expression of one or more
XX cDNAs in a sample, or screening several molecules or compounds to
XX identify a molecule or compound that specifically binds a cDNA of the
XX invention. A protein encoded by the cDNA may be used to screen several
XX molecules or compounds to identify a ligand that specifically binds to
XX the protein, or to produce or purify an antibody to the protein that can
XX be used to detect a protein in a sample or purify a natural or
XX recombinant protein from a sample. The nucleotides may be useful for
XX diagnosing, staging, treating, or monitoring the progression of treatment
XX of a vascular disease, e.g. atherosclerosis, cancer, coronary artery
XX disease, hypertension, diabetes, pre-eclampsia, ischaemia-reperfusion
XX injury, restenosis, or stroke. The cDNAs can also be used for large-scale
XX genetic or gene expression analysis of several new nucleic acid
XX molecules. Antibodies to the proteins encoded by the cDNAs are useful for
XX diagnosing pre-pathologic disorders, and chronic or acute diseases
XX associated with abnormalities in the expression, amount or distribution
XX of the protein. The present sequence represents a cDNA of the invention
XX that is differentially expressed in activated vascular tissue. Note: The
XX sequence data for this patent did not form part of the specification, but
XX was obtained in electronic format directly from USPTO at
XX <http://seqdata.uspto.gov/sequence.html?DocID=20020137081>
XX Sequence 972 BP; 265 A; 228 C; 252 G; 227 T; 0 U; 0 Other;
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XX Query Match 2.0%; Score 74; DB 7; Length 972;
XX Best Local Similarity 67.5%; Pred. No. 7.6e-11;
XX Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
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XX 1307 GCCTGGAGCCCTCCATCTCCAAAGGAGATCATGACCCCTTCCACCACCAAGCACCATCAG 1366
XX 202 GCCTGGAGCCCTCCATCAACCGCGAGATCATGCGAGTGCACACAGCAAGCACCACGGC 261
XX DB

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QY 1367 ACTTATGTTAAACGGCTCAACGCTGCGAGGAGAGCTACTCGCGCGTGTGGCAAGGAG 1426
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262 GCCTACGTGAACAACCTGAACGTCACCGAGAGAGTACCAGGAGGCGTTGGCCAAAGGA 321
QY 1427 GATGTCCTTACCCAGGTTAAGCTTCACTGCTGTGTAC 1460
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
322 GATGTTACAGCCAGATAGCTCTTCAGCCTGCAC 355

RESULT 15
ABL66512
ID ABL66512 standard; DNA; 1026 BP.
XX
AC ABL66512;
XX
DT 15-MAY-2002 (first entry)
DE
DE Lung cancer related gene sequence SEQ ID NO:4849.
XX
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; Gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
KW Gene; ds.
XX
XX Homo sapiens.
XX
XX WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
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PR 28-SEP-2000; 2000US-0236111P.
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PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
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PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
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PR 01-NOV-2000; 2000US-0245084P.
XX
XX (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
XX WPI; 2002-188264/24.
XX
XX Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
XX Claim 1; SEQ ID NO 4849; 44pp; English.
XX
XX The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms'
CC tumour
XX
XX Sequence 1026 BP; 283 A; 216 C; 245 G; 282 T; 0 U; 0 Other;
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Query Match 2.0%; Score 74; DB 6; Length 1026;
Best Local Similarity 67.5%; Pred. No. 7.9e-11;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
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113 GCCTGGAACTCATCATCAACGCGCAGATCATGACCTGCACCAAGCAAGCAACCTACG 172
QY 1367 ACTTATGTTAAACGGCTCAACGCTGCGAGGAGAGTACTCGCGCGTGTGGCAAGGAG 1426
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
173 GCCTACGTGAACAACCTGAACGTCACCGAGGAGAGTACCAGGAGGCGTTGGCCAAAGGA 232
QY 1427 GATGTCCTTACCCAGGTTAAGCTTCACTGCTGTGTAC 1460
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233 GATGTTACAGCCAGATAGCTCTTCAGCCTGCAC 266

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 12:34:16 ; Search time 1266.68 Seconds
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Title: US-09-727-855B-1

Perfect score: 3632

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Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	74	2.0	972	13	US-10-044-090-836
5	74	2.0	986	14	US-10-198-846-13503
6	74	2.0	1026	9	US-09-954-456-1822
7	74	2.0	1026	12	US-10-342-887-509
8	74	2.0	1026	12	US-10-342-887-1305
9	74	2.0	1067	10	US-09-971-429B-22
10	74	2.0	1492	9	US-09-917-800A-1627
11	74	2.0	2825	14	US-10-198-846-13787
12	73	2.0	325	9	US-09-993-333-11
13	72.6	2.0	424	9	US-09-960-352-14744
14	71	2.0	2208	13	US-10-044-090-709
15	69.8	1.9	597	9	US-09-727-855B-6

c	16	68.6	1.9	2809	15	US-10-320-797-25	Sequence 25, Appl
	17	68.2	1.9	894	14	US-10-247-671-122	Sequence 122, App
	18	67.8	1.9	344	10	US-09-918-995-24298	Sequence 24298, A
	19	66.2	1.8	812	14	US-10-109-670-4	Sequence 4, Appli
	20	65.2	1.8	600	9	US-09-738-626-3227	Sequence 3227, Ap
	21	65.2	1.8	1143	9	US-09-818-564-1	Sequence 1, Appli
	22	65.2	1.8	3309400	9	US-09-738-626-1	Sequence 1, Appli
	23	63.6	1.8	630	14	US-10-109-670-29	Sequence 29, Appli
	24	60.8	1.7	3375	9	US-09-727-855B-2	Sequence 2, Appli
	25	60.4	1.7	1984	12	US-10-342-887-267	Sequence 267, App
	26	59	1.6	2217	12	US-10-424-599-90403	Sequence 90403, A
	27	56.8	1.6	6004	10	US-09-960-706-1077	Sequence 1077, Ap
	28	56.8	1.6	6004	10	US-09-873-319-715	Sequence 715, App
	29	56.8	1.6	6004	10	US-09-873-367C-1059	Sequence 1059, Ap
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	31	55.8	1.5	321	12	US-10-085-783A-32727	Sequence 32727, A
	32	55.8	1.5	321	15	US-10-242-535A-32727	Sequence 32727, A
	33	55.8	1.5	376	9	US-09-920-455-67	Sequence 67, Appl
	34	55.8	1.5	477	10	US-09-918-995-16177	Sequence 16177, A
c	35	55.8	1.5	598	14	US-10-029-386-9423	Sequence 9423, Ap
c	36	55.8	1.5	987	12	US-10-424-599-90405	Sequence 90405, A
	37	52.6	1.4	381	9	US-09-960-352-13	Sequence 13, Appl
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c	39	52.6	1.4	413	9	US-09-960-352-5724	Sequence 5724, Ap
c	40	52.6	1.4	425	9	US-09-960-352-5493	Sequence 5493, Ap
	41	52.6	1.4	1295	15	US-10-310-154-294	Sequence 294, App
	42	51.8	1.4	344	11	US-09-864-408A-2105	Sequence 2105, Ap
	43	51.8	1.4	732	14	US-10-230-331-9	Sequence 9, Appli
c	44	51	1.4	264	9	US-09-960-352-4529	Sequence 4529, Ap
c	45	51	1.4	330	9	US-09-960-352-11115	Sequence 11115, A

ALIGNMENTS

RESULT 1

US-09-727-855B-1
; Sequence 1, Application US/09727855B
; Patent No. US20020168703A1
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SITOUCUCHI, Yutaka
; TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUL
; TITLE OF INVENTION: MATERIALS THEREOF
; FILE REFERENCE: C38435/111694
; CURRENT APPLICATION NUMBER: US/09/727,855B
; CURRENT FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: Phaffia rhodozyma
US-09-727-855B-1

Query Match	100.0%;	Score 3632;	DB 9;	Length 3632;
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1441 Db GGTTAAGCTTCAGTCTGTACGTCTGACCGTTTTTTTATCGACCGCAAGCCCTGGTGA 1500
1501 QY GGGAGATGAAGTTTTGATGAGCGCTCATCGTCTAGCACGTTGACCCGATCATACAGGCTCT 1560
1501 Db GGGAGATGAAGTTTTGATGAGCGCTCATCGTCTAGCACGTTGACCCGATCATACAGGCTCT 1560
1561 QY CAAGTTCAACGAGGAGGACACATCAATCGTCAGTGATATTTCTTCAAACTCTTGTGAGC 1620
1561 Db CAAGTTCAACGAGGAGGACACATCAATCGTCAGTGATATTTCTTCAAACTCTTGTGAGC 1620
1621 QY AAGTCAGSTCAAGCTGACTGTTTTGCTTTGTTCTGCGGATCTATCTCATCTCTGATTTG 1680
1621 Db AAGTCAGSTCAAGCTGACTGTTTTGCTTTGTTCTGCGGATCTATCTCATCTCTGATTTG 1680
1681 QY GCATGATGAAACAGACTCTCTGTTCTGGAAGAACTTGGCTCCCTATGATCCGAGAGGC 1740
1681 Db GCATGATGAAACAGACTCTCTGTTCTGGAAGAACTTGGCTCCCTATGATCCGAGAGGC 1740
1741 QY TACCTCTCTCAAGGAGCCTCTCAAGAGGCTATCGAGGAATCTTTTGGTTCTTTCGAGGG 1800
1741 Db TACCTCTCTCAAGGAGCCTCTCAAGAGGCTATCGAGGAATCTTTTGGTTCTTTCGAGGG 1800
1801 QY TCCGTCCATCTATCTTCTCTATTCAGTGTGTTTGGTTCGGGTACTCATCTGTTTGT 1860
1801 Db TCCGTCCATCTATCTTCTCTATTCAGTGTGTTTGGTTCGGGTACTCATCTGTTTGT 1860
1861 QY TCCCCACAAAATAAAAAATAAAAACTTCTCTCCGGGGTTCGACTGCGACTTACATAG 1920
1861 Db TCCCCACAAAATAAAAAATAAAAACTTCTCTCCGGGGTTCGACTGCGACTTACATAG 1920
1921 QY CTTTCAAGAGAGTTCAACGCTGACACCGCTGTCTCAAGGATCCCGATGGGCTGGC 1980
1921 Db CTTTCAAGAGAGTTCAACGCTGACACCGCTGTCTCAAGGATCCCGATGGGCTGGC 1980
1981 QY TTGTATGTATCATATCTCTTCCATCTCAAACTCTCTCAGAGTCTTTTCTTGGAGACTT 2040
1981 Db TTGTATGTATCATATCTCTTCCATCTCAAACTCTCTCAGAGTCTTTTCTTGGAGACTT 2040
2041 QY CAACTGACTATACATGTTTCTTACAAACAAACAGAGGCTTGAACCCGCTTACTAAGAG 2100
2041 Db CAACTGACTATACATGTTTCTTACAAACAAACAGAGGCTTGAACCCGCTTACTAAGAG 2100
2101 QY CTGGAAGTCAACAGACCGCAACAGACCCCTGCTTGTAGTAAGTTGTTCTACATGAT 2160
2101 Db CTGGAAGTCAACAGACCGCAACAGACCCCTGCTTGTAGTAAGTTGTTCTACATGAT 2160
2161 QY TTTCTATCTCAACGGATCTGCATGATTCGTCACCTGATTCTCATGATTTCTTGTTCGT 2220
2161 Db TTTCTATCTCAACGGATCTGCATGATTCGTCACCTGATTCTCATGATTTCTTGTTCGT 2220
2221 QY TTTTCTCGGGATGATTTTCATAAACAGCTCACAATCCTATCATCGGAGTTGACGCTAT 2280
2221 Db TTTTCTCGGGATGATTTTCATAAACAGCTCACAATCCTATCATCGGAGTTGACGCTAT 2280
2281 QY CTTTCTTGAATAGTCTGAGCGTCTGATCTCGTTTTTATTGACGAGTGTGCTTCTGCC 2340
2281 Db CTTTCTTGAATAGTCTGAGCGTCTGATCTCGTTTTTATTGACGAGTGTGCTTCTGCC 2340
2341 QY AAATCATTAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAA 2400
2341 Db AAATCATTAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAA 2400

2401 ACAGCTTTCTACCTTCAAGTCAAGAAAGTCAAGCTGACTATCTCGCTGCTGTTGTTGCTCG 2460
2401 ACAGCTTTCTACCTTCAAGTCAAGAAAGTCAAGCTGACTATCTCGCTGCTGTTGTTGCTCG 2460
2461 TTATCAACTACAAGGAGGAGGCGGCGGATTCAGGCTGCTCTCTAAGCGGGAAGAAAG 2520
2461 TTATCAACTACAAGGAGGAGGCGGCGGATTCAGGCTGCTCTCTAAGCGGGAAGAAAG 2520
2521 TAACGACATATGAAGGAGGAGTCAAAATATCGTTTCTTATAAACAACCTTCGAGGAGAT 2580
2521 TAACGACATATGAAGGAGGAGTCAAAATATCGTTTCTTATAAACAACCTTCGAGGAGAT 2580
2581 GGGAGAGTACGTACAAGAGAGGTTTCTATCGAAATGAGTTTGTGAGCGTTAGCAGGT 2640
2581 GGGAGAGTACGTACAAGAGAGGTTTCTATGGAAATGAGTTTGTGAGCGTTAGCAGGT 2640
2641 TATGATATATGATGATATAGTCTAGTCTAATCTGAAAGAGAGAAACAAGATGTTTGTG 2700
2641 TATGATATATGATGATATAGTCTAGTCTAATCTGAAAGAGAGAAACAAGATGTTTGTG 2700
2701 CGAAGAGATGAGAGATCAAGCCGCTCATCTGATCTGAAACAACATGCCCCCTGCTCG 2760
2701 CGAAGAGATGAGAGATCAAGCCGCTCATCTGATCTGAAACAACATGCCCCCTGCTCG 2760
2761 CAACAGTTTCTAGCATTATGACCATGTTTCATGTTGAAATGGGAAATGAGCCAGAAAG 2820
2761 CAACAGTTTCTAGCATTATGACCATGTTTCATGTTGAAATGGGAAATGAGCCAGAAAG 2820
2821 GTTTATATCTAATTCATTGATTCATGCGACTATGATATGATGATGATGATGATGATGAT 2880
2821 GTTTATATCTAATTCATTGATTCATGCGACTATGATATGATGATGATGATGATGATGAT 2880
2881 ACAGATGCAACAAGACAGCGCATTTTCCAAAGATCGAGTCTCCCAACAAGTATGCGGCA 2940
2881 ACAGATGCAACAAGACAGCGCATTTTCCAAAGATCGAGTCTCCCAACAAGTATGCGGCA 2940
2941 GGTTCCTGTTTAAAGATATATAAAGCAGACGACAAACAAATCGTTTATCGACCCCTGTC 3000
2941 GGTTCCTGTTTAAAGATATATAAAGCAGACGACAAACAAATCGTTTATCGACCCCTGTC 3000
3001 ACCAACACCGTACCGTTTACAGAGTTGTTAGAGTTGTTAGAGTTGTTAGTTGTTAGAG 3060
3001 ACCAACACCGTACCGTTTACAGAGTTGTTAGAGTTGTTAGAGTTGTTAGTTGTTAGAG 3060
3061 TCCAGACTGAGCGCTTCCAAAGCTTCAACAACTTCTCGGAGAGTCTGCTGTTGGGAAAG 3120
3061 TCCAGACTGAGCGCTTCCAAAGCTTCAACAACTTCTCGGAGAGTCTGCTGTTGGGAAAG 3120
3121 AAAAGGCAAAAGGAAACAGAGGATAGATATGATTTCTTCTACTTCTTATAGGCTCTT 3180
3121 AAAAGGCAAAAGGAAACAGAGGATAGATATGATTTCTTCTACTTCTTATAGGCTCTT 3180
3181 AGCTCAAGTCAATCACTACATGTTCTTTGGCGTACCGAAGACGTTCTCAAGCTGCTGTTG 3240
3181 AGCTCAAGTCAATCACTACATGTTCTTTGGCGTACCGAAGACGTTCTCAAGCTGCTGTTG 3240
3241 AAGCTTTTCCGAGCTTCCAGTAGGTTCCCTGTTGGAGAGAGATGTCGAAGGCTTAAGG 3300
3241 AAGCTTTTCCGAGCTTCCAGTAGGTTCCCTGTTGGAGAGAGATGTCGAAGGCTTAAGG 3300
3301 GCGATAAAAGCATGAAGATATTAGTCTATCGGCGCATATAAAGTGTGACGAGATGAAT 3360
3301 GCGATAAAAGCATGAAGATATTAGTCTATCGGCGCATATAAAGTGTGACGAGATGAAT 3360
3361 GGAGAAAAGATGATTCGACCATCGACCTCGACCAAGGAATGAGGTGTCAACCGG 3420
3361 GGAGAAAAGATGATTCGACCATCGACCTCGACCAAGGAATGAGGTGTCAACCGG 3420
3421 CTTCCACTTCTGTTACTCTCAACGTTGACGAAGATGACGAAGCAGTCCGTCGCTTAGC 3480
3421 CTTCCACTTCTGTTACTCTCAACGTTGACGAAGATGACGAAGCAGTCCGTCGCTTAGC 3480

3481 CTCGGCTCGTAGATGCTGATGAACACAAATAGGTAGTAGGAGAGAGAGAAAGATG 3540
3481 CTCGGCTCGTAGATGCTGATGAACACAAATAGGTAGTAGGAGAGAGAGAAAGATG 3540
3541 ATGAGATGTCAGGATGCTTGTCTTACTGTAGATGGAGAGAGATATCGAAGCAAGAC 3600
3541 ATGAGATGTCAGGATGCTTGTCTTACTGTAGATGGAGAGAGATATCGAAGCAAGAC 3600
3601 ATACACTTTTGAAGAGCTTGAACCAATTTAG 3632
3601 ATACACTTTTGAAGAGCTTGAACCAATTTAG 3632

RESULT 2
US-09-727-855B-4
; Sequence 4, Application US/09727855B
; Patent No. US20020168703A1
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUL
; TITLE OF INVENTION: MATERIALS THEREOF
; FILE REFERENCE: C38435/111694
; CURRENT APPLICATION NUMBER: US/09/727,855B
; CURRENT FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Phaffia rhodozyma
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(666)
; OTHER INFORMATION: n or X = A, C, G or T
US-09-727-855B-4

Query Match 4.2%; Score 151.4; DB 9; Length 669;
Best Local Similarity 99.3%; Pred. No. 9.7e-36;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

31305 AGGCTCTGAGCGCTTCCATCTCCAGGAGATCATGACCTTCCACACACCAAGCACCATC 1364
110 ATGCTCTGAGCGCTTCCATCTCCAGGAGATCATGACCTTCCACACACCAAGCACCATC 169
1365 AGACTTATTTAAACGGCTTCAACGCTGCGAGGAGAGTCTCGGCGCTGTGGGCAAG 1424
170 AGACTTATTTAAACGGCTTCAACGCTGCGAGGAGAGTCTCGGCGCTGTGGGCAAG 229
1425 AGGATGCTGTTACCCAGGTTAAGCTTCACTCTG 1457
230 AGGATGCTGTTACCCAGGTTAAGCTTCACTCTG 262

RESULT 3
US-10-109-670-3
; Sequence 3, Application US/10109670
; Publication No. US20030105283A1
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH et al.
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA
; FILE REFERENCE: 1422-0523P
; CURRENT APPLICATION NUMBER: US/10/109,670
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 3
; LENGTH: 728
; TYPE: DNA
; ORGANISM: Malassezia furfur
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(728)

OTHER INFORMATION: Strandedness:double-Topology:linear-Molecule Type:cdna to mRNA
US-10-109-670-3

Query Match 2.3%; Score 84.2; DB 14; Length 728;
Best Local Similarity 71.9%; Pred. No. 1.1e-14;
Matches 110; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
QY 1305 AGCCCTGGAGCCCTCCATCTCCAGGAGATCATGACCCCTTCCACACCAAGCACCATC 1364
DB 50 ATGGCTGGAGCCGTTTACTTAAAGAGATCATGACGTCACACCAAGCACCATC 109
QY 1365 AGACTTATGTTAAAGCCCTCAACGTCGCCGAGGAGCTACTCGGCCCTGTGGCAAGG 1424
DB 110 AGACTTATGTTAAAGCCCTCAACGTCGCCGAGGAGCTACTCGGCCCTGTGGCAAGG 169
QY 1425 AGGATGTCCTTACCAGGTTAAGCTTCACTGTG 1457
DB 170 ACAGCTGTCCTTAAAGCAGATCCAGCTGCAGAGTG 202

RESULT 4
US-10-044-090-836
Sequence 836, Application US/10044090
Publication No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 836
LENGTH: 972
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 010001CB1
US-10-044-090-836

Query Match 2.0%; Score 74; DB 13; Length 972;
Best Local Similarity 67.5%; Pred. No. 2.1e-11;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1307 GCCCTGGAGCCCTCCATCTCCAGGAGATCATGACCCCTTCCACCAAGCACCATCAG 1366
DB 202 GCCCTGGAGCCCTCCATCTCCAGGAGATCATGACCCCTTCCACCAAGCACCATCAG 261
QY 1367 ACTTATGTTAAAGCCCTCAACGTCGCCGAGGAGCTACTCGGCCCTGTGGCAAGGAG 1426
DB 262 GCCTACGTGAACACCTGAAGTCAACGAGGAGTACAGGAGGAGTACAGGAGGCGTTGCCAAGGA 321
QY 1427 GATGTGTTACCGAGTTAAGCTTCACTGTGTAC 1460
DB 322 GATGTGTTACCGAGTACGCTTCTCAGCCTGCAC 355

RESULT 5
US-10-198-846-13503
Sequence 13503, Application US/10198846
Publication No. US2003009974A1
GENERAL INFORMATION:
APPLICANT: Xue, Yongyao
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13503
LENGTH: 996
TYPE: DNA
ORGANISM: Homo sapiens
US-10-198-846-13503

Query Match 2.0%; Score 74; DB 14; Length 996;
Best Local Similarity 67.5%; Pred. No. 2.1e-11;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1307 GCCCTGGAGCCCTCCATCTCCAGGAGATCATGACCCCTTCCACCAAGCACCATCAG 1366
DB 199 GCCCTGGAGCCCTCCATCTCCAGGAGATCATGACCCCTTCCACCAAGCACCATCAG 258
QY 1367 ACTTATGTTAAAGCCCTCAACGTCGCCGAGGAGCTACTCGGCCCTGTGGCAAGGAG 1426
DB 259 GCCTACGTGAACAACTCAACGTCGCCGAGGAGTACCAAGGAGGCGTTGCCCAAGGA 318
QY 1427 GATGTGTTACCGAGTTAAGCTTCACTGTGTAC 1460
DB 319 GATGTGTTACCGAGTACGCTTCTCAGCCTGCAC 352

RESULT 6
US-09-954-456-1822
Sequence 1822, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: Patent version 3.0
SEQ ID NO 1822
LENGTH: 1026
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-1822

Query Match 2.0%; Score 74; DB 9; Length 1026;
Best Local Similarity 67.5%; Pred. No. 2.2e-11;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1307 GCCCTGGAGCCCTCCATCTCCAGGAGATCATGACCCCTTCCACCAAGCACCATCAG 1366
DB 113 GCCCTGGAGCCCTCCATCTCCAGGAGATCATGACCCCTTCCACCAAGCACCATCAG 172

1367	ACTATGTTTAAACCGCCTCAACGCTGCCGAGAGAGACTACTCGGCCGCTGTGGCGCAAGAG	1426
Qy		
173	GCCTACGTGAACAACTTGAACGTCACCGAGAGAGTACACGAGGAGCGTTTGGCCAAAGGA	232
Db		
1427	GATGTGTTTACCCAGGTTAAGCTTCAGTCTGTAC	1460
Qy		
233	GATGTTTACAGCCAGATAGTCTTTCAGCTGCAC	266
Db		

RESULT 7

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US-10-342-887-509
; Sequence 509, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 509
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-509

```

	Query Match	2.0%;	Score 74;	DB 12;	Length 1026;
	Best Local Similarity	67.5%;	Pred. No. 2.2e-11;		
	Matches 104;	Conservative 0;	Mismatches 50;	Indels 0;	Gaps 0;
QY	1307	GCCTCGAGCCCTCCATCTCCAAAGGAGATCATACCTTCACACACCAAGCAGCACTCAG	1366		
Db	113	GCCTGGAACTCTACATCAACGGCGAGATCATCGCTGCACACCAAGCAGCACCACGC	172		
QY	1367	ACTTATGTTTAAGGGCCTCAACGCTGCCGAGGAGAGTACTCGGCCGCTGTGGCCAAAGGAG	1426		
Db	173	GCCTAGTGAACAACTGAACGTCACCGAGGAGAGTACCAGGAGGGGTGGCCAAAGGA	232		
QY	1427	GATGTGCTTACCGAGGTTAAGCTTCAGTCTGTATC	1460		
Db	233	GATGTTACAGCCAGATAGCTCTTCACTGCTGCAC	266		

RESULT 8

US-10-342-887-1905
; Sequence 1905, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342-887

```

; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1905
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1905

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	Query Match	2.0%;	Score 74;	DB 12;	Length 1026;
	Best Local Similarity	67.5%;	Pred. No. 2.2e-11;		
	Matches 104;	Conservative 0;	Mismatches 50;	Indels 0;	Gaps 0;
QY	1307	GCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCTTCACACACACCAAGCACCATCAG	1366		
Db	113	GCCTTGGALCCTCACATCAACGGCGAGATCATGAGCTGCACCACCAAGCACCACGCG	172		
QY	1367	ACTTATGTGTTAAACGGCCTCAACGCTGCGCGAGGAGAGCTACTCGGCCGCTGTGGGCCAAAGGAG	1426		
Db	173	GCCTACGTGAACAACCTGAACGTCAACGAGGAGAAGTACCAGGAGGCGTTGGCCCAAGGA	232		
QY	1427	GATGTGCTTACCCAGGTGTTAAGCTTCAGTCTGTATAC	1460		
Db	233	GATGTTTACAGCCACGATAGCTCTTTCACGCTGAC	266		

RESULTS

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US-09-971-429B-22
; Sequence 22, Application US/09971429B
; Publication No. US20030175704A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K. W.
; APPLICANT: Shujan, Andrew W.
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0040 US
; CURRENT APPLICATION NUMBER: US/09/971,429B
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/239,024
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PERL Program
; SEQ ID NO 22
; LENGTH: 1067
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030175704A1 241107.19
US-09-971-429B-22

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	Query Match	2.0%;	Score 74;	DB 10;	Length 1067;
	Best Local Similarity	67.5%;	Pred. No. 2.2e-11;		
	Matches 104;	Conservative 0;	Mismatches 50;	Indels 0;	Gaps 0;
QY	1307	GCCTTGGAGCCCTCCATCTCCAAGGAGATCATGACCTTCACACACCAAGCACCATCAG	1366		
Db	272	GCCTTGGAACTTCATCAACCGGCAGATCATGAGCTGCACACAGCAAGCACCAACGCG	331		
QY	1367	ACTTATGTTAAAGGGCTCAACGCTGCCAGGAGAGCTACTCGGCCGCTGTGGCCAGGAG	1426		
Db	332	GCCTACGTGAACAACCTGACGTACCGAGGAGAGTACCGAGGCGCTTGGCCACAGGA	391		
QY	1427	GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC	1460		
Db	392	GATGTTACAGCCAGATAGCTCTCAGCCTGCAC	425		


```

; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Mengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 14744
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 63-LIB3057-022-Q1-K1-H4
US-09-960-352-14744

Query Match      2.0%; Score 72.6; DB 9; Length 424;
Best Local Similarity 67.5%; Pred. No. 3e-11;
Matches 102; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1307 GCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCTTCACACACCAAGCACCATCAG 1366
Db 157 GCCTGGAGCCGCGACATCAACGCGCAGATCATGCGCTGCACCAAGCACCACCGC 216

QY 1367 ACTATGTTAAACGGCTCAACGCTGCCGAGGAGAGCTACTCGCGCGCTGCGCAAGGAG 1426
Db 217 GCCTAGTGAACCTCAACGCTGCCGAGGAGAGTACCGGAGGCGCTGGAGAAGGCT 276

QY 1427 GATGCTTACCAGGTTAAGCTTCAAGTCTG 1457
Db 277 GATGTTACAGCTCAGATAGCTCTGCAGCCTG 307

RESULT 14
US-10-044-090-709
; Sequence 709, Application US/10044090
; Publication No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 709
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: InCyte ID No. US20020137081A1 241107.13
US-10-044-090-709

Query Match      2.0%; Score 71; DB 13; Length 2208;
Best Local Similarity 66.9%; Pred. No. 3.4e-10;
Matches 101; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1310 CTGGAGCCCTCCATCTCCAAGGAGATCATGACCTTCACACCAAGCACCACCATCAGACT 1369
Db 117 CTGGAACCTTCACATCAACGCGCAGATCATGCGCTGCACCAAGCAGCAGCACCACGCGCC 176

QY 1370 TATGTTAAGCGCTCAACGCTGCCGAGGAGAGTACTCGGCGCGCTGTGGCAAGGAGGAT 1429
Db 177 TAGTGAAACAACCTGAACCTGACCGAGGAGAGTACCAGAGGCGCTTGGCCCAAGGAGAT 236

QY 1430 GTGCTTACCCAGGTTAAGCTTCAAGTCTGATC 1460
Db 237 GTTACAGCCCCAGATAGCTCTTTCAGCCTGCAC 267

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RESULT 15
US-09-727-855B-6
; Sequence 6, Application US/09727855B
; Patent No. US20020168703A1
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUL
; FILE OF INVENTION: MATERIALS THEREOF
; FILE REFERENCE: C38435/111694
; CURRENT APPLICATION NUMBER: US/09/727,855B
; CURRENT FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(594)
; OTHER INFORMATION:
US-09-727-855B-6

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Search completed: April 1, 2004, 14:10:44
Job time : 1277.68 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 12:35:05 ; Search time 14031.5 Seconds
(without alignments)
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Title: US-09-727-855B-1

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Scoring table: IDENTITY NUC

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Searched: 3470272 seqs, 21671516995 residues

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Minimum DB seq length: 0

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Listing first 45 summaries

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ALIGNMENTS

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DEFINITION Sequence 1 from Patent EP1111067.
ACCESSION AX128476
VERSION AX128476.1 GI:14134943
KEYWORDS
SOURCE
ORGANISM
Xanthophyllomyces dendrorhous (anamorph: Phaffia rhodozyma)
Xanthophyllomyces dendrorhous
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Cystofilobasidiales;
Cystofilobasidiaceae; Xanthophyllomyces.
REFERENCE
AUTHORS Hoshino, T., Ojima, K. and Setoguchi, Y.
TITLE Recombinant production of carotenoids, particularly astaxanthin

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LOCUS

BD015710

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PAT 27-AUG-2002

Recombination production of carotenoids, in particular,

astaxanthin.

ACCESSION

BD015710

VERSION

BD015710.1

GI:22556847

JP 2001190294-A/1.

KEYWORDS

Xanthophyllomycetes dendrorhous

Xanthophyllomycetes dendrorhous

Eukaryota; Fungi; Basidiomycota; Hymenomycetes;

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Cystofilobasidiales; Xanthophyllomycetes.

1 (bases 1 to 3632)

REFERENCE

1 (bases 1 to 3632)

AUTHORS

Hoshino, T., Ojima, K. and Setoguchi, Y.

Recombination production of carotenoids, in particular, astaxanthin
Patent: JP 2001190294-A 1 17-JUL-2001;
F HOFFMANN LA ROCHE AG
OS Phaffia rhodozyma
PN JP 2001190294-A/1
PD 17-JUL-2001
PF 01-DEC-2000 JP 2000367099
PR 01-DEC-1999 EP 99123821.3
PI TATSUO HOSHINO, KAZUYUKI OJIMA, YUTAKA SETOYUCHI PC
C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12P23/00, C12Q1/68// PC
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LOCUS

DEFINITION Sequence 4 from Patent EP1111067.

AX128479 669 bp DNA linear PAT 15-MAY-2001

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ORIGIN
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Matches 96; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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RESULT 9
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DEFINITION
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VERSION     Z18857.1 GI:288504
KEYWORDS   manganese superoxide dismutase.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 779)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE     Hallowell, R.A., Mullenbach, G.T., Stempien, M.M. and Bell, G.I.
MEDLINE   Sequence of a cDNA coding for mouse manganese superoxide dismutase
PUBMED    Nucleic Acids Res. 14 (23), 9539 (1986)
87091590
3797253

REFERENCE  2 (bases 1 to 779)
AUTHORS   Sun, Y., Hegamyer, G. and Colburn, N.H.
JOURNAL   Sequence of manganese superoxide dismutase-encoding cDNAs from
TITLE     multiple mouse organs
MEDLINE   Gene 131 (2), 301-302 (1993)
PUBMED    8406027

REFERENCE  3 (bases 1 to 779)
AUTHORS   Sun, Y.
JOURNAL   Direct Submission
TITLE     Submitted (25-NOV-1992) Sun Y., FCRDC, CBS, LVC, P.O. Box B,
PUBMED    Frederick, MD, 21702-1201

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Db 144 GCCTGGAGCCACACATTAACGGCGAGATCATGAGCTGCACACAGCAGCACCATCGG 203
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Db 204 GCCTACGTGAACAACCTCAACGCCACCGAGGAGAGTACCACGAGGCTCTGGCCAAGGGA 263
QY 1427 GATGTGCTTACCAGGTTAAGCTTCAGTCTGTAC 1460
Db 264 GATGTTACAACCTCAGGTCGCTCTTCAGCCTGCAC 297

RESULT 10
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ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 897)
AUTHORS   Hallowell, R.A., Mullenbach, G.T., Stempien, M.M. and Bell, G.I.
JOURNAL   Sequence of a cDNA coding for mouse manganese superoxide dismutase
TITLE     Nucleic Acids Res. 14 (23), 9539 (1986)
MEDLINE   87091590
PUBMED    3797253

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 ACCESSION AB087277
 VERSION AB087277.1 GI:23503531
 KEYWORDS
 SOURCE Macaca fuscata (Japanese macaque)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 Cercopitheciinae; Macaca.

REFERENCE
 AUTHORS Fukuhara,R., Tezuka,T. and Kageyama,T.
 TITLE Structure, molecular evolution, and gene expression of primate superoxide dismutases
 JOURNAL Gene 296, 99-109 (2002)
 REFERENCE
 AUTHORS Fukuhara,R. and Kageyama,T.
 TITLE Direct Submission
 JOURNAL Submitted (02-JUL-2002) Ryoji Fukuhara, Primate Research Institute, Kyoto University, Center for Human Evolution Modeling Research, Kanrin, Inuyama, Aichi 484-8506, Japan
 (E-mail:fukuhara@pri.kyoto-u.ac.jp, Tel:81-568-63-0578, Fax:81-568-63-0085)

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RESULT 12
 AB087278
 LOCUS
 DEFINITION Macaca fascicularis mRNA for Mn-superoxide dismutase, complete cds.
 ACCESSION AB087278
 VERSION AB087278.1 GI:23503533
 KEYWORDS
 SOURCE Macaca fascicularis (crab-eating macaque)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 Cercopitheciinae; Macaca.

REFERENCE
 AUTHORS Fukuhara,R., Tezuka,T. and Kageyama,T.
 TITLE Structure, molecular evolution, and gene expression of primate superoxide dismutases
 JOURNAL Gene 296, 99-109 (2002)
 REFERENCE
 AUTHORS Fukuhara,R. and Kageyama,T.
 TITLE Direct Submission
 JOURNAL Submitted (02-JUL-2002) Ryoji Fukuhara, Primate Research Institute, Kyoto University, Center for Human Evolution Modeling Research, Kanrin, Inuyama, Aichi 484-8506, Japan
 (E-mail:fukuhara@pri.kyoto-u.ac.jp, Tel:81-568-63-0578, Fax:81-568-63-0085)

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 Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 Cercopitheciinae; Macaca.

REFERENCE
 AUTHORS Fukuhara,R., Tezuka,T. and Kageyama,T.
 TITLE Structure, molecular evolution, and gene expression of primate superoxide dismutases
 JOURNAL Gene 296, 99-109 (2002)
 REFERENCE
 AUTHORS Fukuhara,R. and Kageyama,T.
 TITLE Direct Submission
 JOURNAL Submitted (02-JUL-2002) Ryoji Fukuhara, Primate Research Institute, Kyoto University, Center for Human Evolution Modeling Research, Kanrin, Inuyama, Aichi 484-8506, Japan
 (E-mail:fukuhara@pri.kyoto-u.ac.jp, Tel:81-568-63-0578, Fax:81-568-63-0085)

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RESULT 13
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 Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 Cercopitheciinae; Macaca.

REFERENCE
 AUTHORS Fukuhara,R., Tezuka,T. and Kageyama,T.
 TITLE Structure, molecular evolution, and gene expression of primate superoxide dismutases
 JOURNAL Gene 296, 99-109 (2002)
 REFERENCE
 AUTHORS Fukuhara,R. and Kageyama,T.
 TITLE Direct Submission
 JOURNAL Submitted (02-JUL-2002) Ryoji Fukuhara, Primate Research Institute, Kyoto University, Center for Human Evolution Modeling Research, Kanrin, Inuyama, Aichi 484-8506, Japan
 (E-mail:fukuhara@pri.kyoto-u.ac.jp, Tel:81-568-63-0578, Fax:81-568-63-0085)


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  SOURCE
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    Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
  REFERENCE
    1 Fukuhara,R., Tezuka,T. and Kageyama,T.
      Structure, molecular evolution, and gene expression of primate
      superoxide dismutases
      Gene 296, 99-109 (2002)
  JOURNAL
    2 (bases 1 to 600)
  REFERENCE
    Fukuhara,R. and Kageyama,T.
    Direct Submission
    Submitted (02-JUL-2002) Ryoji Fukuhara, Primate Research Institute,
    Kyoto University, Center for Human Evolution Modeling Research;
    Kanrin, Inuyama, Aichi 484-8506, Japan
    (E-mail:fukuhara@pri.kyoto-u.ac.jp, Tel:81-568-63-0578,
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  REFERENCE
    1 (sites)
    Ishida,N., Katayama,Y., Sato,F., Hasegawa,T. and Mukoyama,H.
    The cDNA sequences of equine antioxidant enzyme genes Cu/Zn-SOD
    and Mn-SOD, and these expressions in equine tissues
    J. Vet. Med. Sci. 61 (3), 291-294 (1999)
  JOURNAL
    99261591
    MEDLINE
    PUBMED
    10331206
  REFERENCE
    2 (bases 1 to 954)
  JOURNAL
    Direct Submission
    Submitted (07-MAR-1997) Nobushige Ishida, JRA Equine Research
    Institute, Laboratory of Molecular and Cellular Biology; 321-4,
    Tokami-cho, Utsunomiya, Tochigi 320-0856, Japan
    (E-mail:noishida@center.equinist.go.jp, Tel:81-28-647-0662,
    Fax:81-28-647-0686)
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 13:12:34 ; Search time 9327 Seconds
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11628.541 Million cell updates/sec

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Searched: 27513289 seqs, 14931090276 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

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29: gb_gsal2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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10	78.8	2.2	372	13	BY300950
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12	78.8	2.2	511	12	BG04894
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14	78.8	2.2	580	12	BI713308
15	78.8	2.2	589	13	BU743935
16	78.8	2.2	689	12	BI526549
17	78.8	2.2	710	10	BF607468
18	78.8	2.2	730	12	BI904486
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21	77.4	2.1	606	14	CA352127
22	77.4	2.1	607	14	CA387190
23	77.4	2.1	622	13	EX076652
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34	76.2	2.1	416	13	BY273152
35	75.8	2.1	475	12	BJ490136
36	75.8	2.1	604	12	BJ491899
37	75.8	2.1	640	9	AU170704
38	75.8	2.1	643	9	AU169164
39	75.6	2.1	332	13	BY334907
40	75.6	2.1	357	13	BY041846
41	75.6	2.1	358	13	BY085746
42	75.6	2.1	358	13	BY163920
43	75.6	2.1	368	13	BY072632
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ALIGNMENTS

RESULT 1	CF192114	333 bp	mRNA	linear	EST 08-AUG-2003
LOCUS	13917j2.r1	Cryptococcus neoformans strain B3501	Cryptococcus		
DEFINITION	neoformans var. neoformans cDNA clone l3917j2 5', mRNA sequence.				
ACCESSION	CF192114				
VERSION	CF192114.1	GI:33513983			
KEYWORDS	EST.				
SOURCE	Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)				
ORGANISM	Cryptococcus neoformans var. neoformans				
REFERENCE	Eukaryota; Fungi; Basidiomycota; Hymenomycetes;				
AUTHORS	Filobasidiella.				
TITLE	1 (bases 1 to 333)				
JOURNAL	Kupfer,D.M., Drabenstot,S.D., Buchanan,K.L., Lai,H., Dyer,D.W.,				
COMMENT	Roe,B.A. and Murphy,J.W.				
	Comparison of highly conserved intronic and exonic elements				
	associated with splicing among five diverse fungal organisms				
	Unpublished (2003)				
	Other ESTs: l3917j2.f1				
	Contact: Murphy, JW				
	Department of Microbiology and Immunology				
	University of Oklahoma Health Sciences Center				
	Oklahoma City, OK 73190, USA				
	Tel: 405-271-2133 ex2133				
	Email: Juneann-murphy@ouhsc.edu				

This clone is available from the Fungal Genetics Stock Center,
Phone 913-588-7044, <http://www.fgsc.net/> Contact Dr. Bruce Roe
(broe@ou.edu, www.genome.ou.edu) for sequencing questions Contact
Dr. Juneann Murphy (juneann-murphy@ouhsc.edu) for library
information.

Seq primer: T3
High quality sequence stop: 327.

FEATURES

Location/Qualifiers

1..333

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

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/db_xref="taxon:40410"

/clone="j5k07j2"

/lab_host="E. coli strain SOLR"

/clone_lib="Cryptococcus neoformans strain B3501"

/note="Vector: pBluescript sk-; Site_1: EcoRI at 5' end of

cDNA insert; Site_2: XhoI at 3' end of cDNA insert"

ORIGIN

Query Match 2.3%; Score 85; DB 14; Length 333;
Best Local Similarity 77.4%; Pred. No. le-08;
Matches 103; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 2389 AGATCTGGGACGCGTTTCTACCTTCAGTACAGAGCGTCAAGCGCTGACTATCTCGCTG 2448

Db 200 ACATCTGGGACGCGTTTCTATCTCCAGTACAGAGCGTCAAGCGCGCTGACTATCTCAATG 259

Qy 2449 CTGTTTGTCGCTTATCAACTACAGGAGGAGGCGCCGATTCGAGGCTGCTCTCTAAG 2508

Db 260 CCACTCGAATGTATCAACTACGAGGAGGCGGAAAGTCGTCTCAAGGCTGCTCAGTAAG 319

Qy 2509 CGGACGAAAGT 2521

Db 320 CTTTATGAACAAT 332

RESULT 2

CF186948/c 388 bp mRNA linear EST 08-AUG-2003

LOCUS

j5k07j2.f1 Cryptococcus neoformans strain B3501 Cryptococcus

neoformans var. neoformans cDNA clone j5k07j2 3', mRNA sequence.

DEFINITION

CF186948

ACCESSION

VERSION

KEYWORDS

SOURCE

Cryptococcus neoformans var. neoformans (Filobasidiella neoformans

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Comparison of highly conserved intronic and exonic elements

associated with splicing among five diverse fungal organisms

Unpublished (2003)

Other ESTs: j5k07j2.r1

Contact: Murphy, JW

Department of Microbiology and Immunology

University of Oklahoma Health Sciences Center

Oklahoma City, OK 73190, USA

Tel: 405-271-2133 ex2133

Email: juneann-murphy@ouhsc.edu

This clone is available from the Fungal Genetics Stock Center,

Phone 913-588-7044, <http://www.fgsc.net/> Contact Dr. Bruce Roe

(broe@ou.edu, www.genome.ou.edu) for sequencing questions Contact

Dr. Juneann Murphy (juneann-murphy@ouhsc.edu) for library

information.

Seq primer: M13-20

High quality sequence stop: 379.

Location/Qualifiers

1..388

FEATURES

source

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

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/db_xref="taxon:40410"

/clone="j5k07j2"

/lab_host="E. coli strain SOLR"

/clone_lib="Cryptococcus neoformans strain B3501"

/note="Vector: pBluescript sk-; Site_1: EcoRI at 5' end of

cDNA insert; Site_2: XhoI at 3' end of cDNA insert"

ORIGIN

Query Match 2.3%; Score 85; DB 14; Length 388;
Best Local Similarity 77.4%; Pred. No. le-08;
Matches 103; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 2389 AGATCTGGGACGCGTTTCTACCTTCAGTACAGAGCGTCAAGCGCTGACTATCTCGCTG 2448

Db 200 ACATCTGGGACGCGTTTCTATCTCCAGTACAGAGCGTCAAGCGCGCTGACTATCTCAATG 141

Qy 2449 CTGTTTGTCGCTTATCAACTACAGGAGGAGGCGCCGATTCGAGGCTGCTCTCTAAG 2508

Db 140 CCACTCGAATGTATCAACTACGAGGAGGCGGAAAGTCGTCTCAAGGCTGCTCAGTAAG 81

Qy 2509 CGGACGAAAGT 2521

Db 80 CTTTATGAACAAT 68

RESULT 3

CF192113/c

LOCUS

DEFINITION

CF192113

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Cryptococcus neoformans var. neoformans

Eukaryota; Fungi; Basidiomycota; Hymenomycetes;

Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;

Filobasidiella.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Comparison of highly conserved intronic and exonic elements

associated with splicing among five diverse fungal organisms

Unpublished (2003)

Other ESTs: 13917j2.r1

Contact: Murphy, JW

Department of Microbiology and Immunology

University of Oklahoma Health Sciences Center

Oklahoma City, OK 73190, USA

Tel: 405-271-2133 ex2133

Email: juneann-murphy@ouhsc.edu

This clone is available from the Fungal Genetics Stock Center,

Phone 913-588-7044, <http://www.fgsc.net/> Contact Dr. Bruce Roe

(broe@ou.edu, www.genome.ou.edu) for sequencing questions Contact

Dr. Juneann Murphy (juneann-murphy@ouhsc.edu) for library

information.

Seq primer: M13-20.

Location/Qualifiers

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/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

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/db_xref="taxon:40410"

/clone="13917j2"

/lab_host="E. coli strain SOLR"

/clone_lib="Cryptococcus neoformans strain B3501"

/note="Vector: pBluescript sk-; Site_1: EcoRI at 5' end of

cDNA insert; Site_2: XhoI at 3' end of cDNA insert"

ORIGIN

Email: alzaatreh@uwaterloo.ca
URL: <http://www.alzaatreh.com>
Aizawa

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FEATURES
source
ccq filename Location/Qualifiers
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/mol_type="mRNA"
/strain="ICR"
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/sex="Both"
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/dev_stage="Embryonic day 16.5"
/lab_host="TOP10"
/clone_lib="Melton Mouse E16 5 pancreas Library 2 M16B2"
/note="Organ: pancreas; Vector: pBluescript II SK; Site 1
Not1; Site 2: SalI; Library constructed using SuperScript
Plasmid Library kit (Life Technologies). cDNA made by
oligo-dt priming.Size-selected by column fractionation;
average insert size 1.06kb. Primary library,"

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FEATURES
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ccq filename Location/Qualifiers
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/organism="Mus musculus"
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/lab_host="TOP10"
/clone_lib="Melton Mouse E16 5 pancreas Library 2 M16B2"
/note="Organ: pancreas; Vector: pBluescript II SK; Site 1
Not1; Site 2: SalI; Library constructed using SuperScript
Plasmid Library kit (Life Technologies). cDNA made by
oligo-dt priming.Size-selected by column fractionation;
average insert size 1.06kb. Primary library,"

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unamplified."

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ORIGIN
Query Match      2.2%; Score 78.8; DB 13; Length 359;
Best Local Similarity 69.5%; Pred. No. 2.8e-07;
Matches 107; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1307 GCCCTGGAGGCGCTCATCTCCAAAGGAGATCATGACCTTCACCAAGAGACCATCAG 1366
Db 104 CGCTGGAGCCACACATTAACGCGCAGATCATGCGTGCACCAAGACCATCGC 163

QY 1367 ACTTATGTTACGGCTCAACGCTCCGAGAGAGGCTACTCGGCGCTGTGGCAAGGAG 1426
Db 164 GCCTACGTGAACACCTCAACGCCACGAGAGAGTACCACGAGGCTCTGGCCAAAGGA 223

QY 1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
Db 224 GATGTACAACTCAGTTCGCTTCACGCTGCAC 257

RESULT 7
BY315073 359 bp mRNA linear EST 11-DEC-2002
LOCUS
DEFINITION
musculus cDNA clone I420017L02 5', mRNA sequence.
ACCESSION
BY315073
VERSION
BY315073.1 GI:26505410
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 359)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamataka,I.,
Kiyosawa,H., Yagi,K., Tonaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojohori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.S., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
Kawaji,H., Kawasawa,Y., Kedierski,R.M., King,B.L., Konagaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maitais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
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Santelin,A., Schneider,C., Sempile,C.A., Setou,M., Shimada,K.,
Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
Verardo,R., Wagner,L., Wahlstedt,C., Wang,Y., Watanabe,Y.,
Wells,C., Wilming,L.G., Wyshaw-Boris,A., Yanagisawa,M., Yang,I.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
12466851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,

FEATURES
source
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/db_xref="taxon:10090"
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/cell_type="osteoclast-like cell"
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cell"

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Query Match      2.2%; Score 78.8; DB 13; Length 359;
Best Local Similarity 69.5%; Pred. No. 2.8e-07;
Matches 107; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1307 GCCCTGGAGGCGCTCATCTCCAAAGGAGATCATGACCTTCACCAAGAGACCATCAG 1366
Db 174 CGCTGGAGCCACACATTAACGCGCAGATCATGACCTGCACCAAGACCATCGC 233

QY 1367 ACTTATGTTACGGCTCAACGCTCCGAGAGAGGCTACTCGGCGCTGTGGCAAGGAG 1426
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QY 1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
Db 294 GATGTACAACTCAGTTCGCTTCACGCTGCAC 327

RESULT 8
BB856053 362 bp mRNA linear EST 26-NOV-2001
LOCUS
DEFINITION
cDNA clone G370031F20 5', mRNA sequence.
ACCESSION
BB856053
VERSION
BB856053.1 GI:17097507
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 362)
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,
Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,

URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
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Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Takashi Ishikawa (Department of Surgery
2 Yokohama City University 3-9 Fukuura, Kanazawa-Ku, Yokohama
236-0004 Japan) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

```

Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sakaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akaira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
 RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2001)
 Unpublished (2001)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp/
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.
 e mouse tissues.
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 ORIGIN
 Query Match 2.2%; Score 78.8; DB 10; Length 362;
 Best Local Similarity 69.5%; Pred. No. 2.8e-07;
 Matches 107; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

 QY 1307 GCCTGGAGCCCTCCATCTCCAGGAGATCATGACCTTTCCACACCAAGCACCATCAG 1366
 Db 198 GCGCTGGAGCCACACATTAAACGCGAGATCATGACCTGCACACAGCAAGCACCATGCG 257
 QY 1367 ACTTATGTTAAAGCGCTCAACGCTGCCGAGGAGAGTACTCGGCCCTGTGGCCAGGAG 1426
 Db 258 GCCTACGTGAACAACCTCAACGCCACCGAGGAGAGTACCACGAGGCTCTGGCCAAAGGGA 317
 QY 1427 GATGTCCTTACCAGGTTAAGCTTACCTCTGTAC 1460
 Db 318 GATGTTTACAACCTACGTCGCTCTTCAGCCCTGCAC 351

 RESULT 9
 BY310981 363 bp mRNA linear EST 11-DEC-2002
 LOCUS BY310981 RIKEN full-length enriched, stroma cell Mus musculus cDNA
 DEFINITION clone I320017112 5', mRNA sequence.
 ACCESSION BY310981
 VERSION BY310981.1 GI:26501318

KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 363)
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Magoshima, T., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Favan, W. J., Perte, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J. C., Reid, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kitahara, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 12466851
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp/
 URL: http://genome.gsc.riken.go.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Tissues were provided by Takashi Ishikawa (Department of Surgery 2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama 236-0004 Japan) whose assistance we gratefully acknowledge.
 Please visit our web site (<http://genome.gsc.riken.go.jp/>) for

FEATURES source

further details.
 Location/Qualifiers
 1. 363
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="1320017112"
 /cell_type="stroma cell"
 /clone_lib="RIKEN full-length enriched, stroma cell"

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 Best Local Similarity 69.5%; Pred. No. 2.8e-07;
 Matches 107; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1307 GCCTGGAGCCCTCATCTCCAGGAGATCATGACCTTACACACAGCACCATCAG 1366
 Db 194 GCGCTGGAGCCACATTAACGCGCAGATCATGCGCTGCACCAAGCACCATGCG 253
 QY 1367 ACTTATGTTAAACGGCTCAACGGTGGCGGAGAGAGTACTCGGCGGTGGGCAAGGAG 1426
 Db 254 GCCTACGTGAACACCTCAACGCCACGAGGAGAGTACACAGGCTCTGGCCAAAGGA 313
 QY 1427 GATGTGTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
 Db 314 GATGTTACAACCTCAGGTGCGCTCTTCAGCTGCAC 347

BY300950 372 bp mRNA linear EST 11-DEC-2002
 RY300950 RIKEN full-length enriched, 14.5 days embryo RP/+
 Rathke's pouches Mus musculus cDNA clone K720012M21 5', mRNA
 sequence.
 BY300950
 BY300950.1 GI:26491287
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
 1 (bases 1 to 372)
 Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
 Nikaide,I., Osato,N., Saito,R., Suzuki,H., Yamana,K., I.,
 Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
 Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Sult,C.,
 Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
 Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
 Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
 Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
 Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
 Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
 Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
 Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
 Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
 Numata,K., Okido,T., Pavan,W.J., Perle,G., Pesole,G.,
 Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
 Ravasi,T., Read,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
 Sultana,R., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
 Verardo,R., Wagner,L., Wahlstedt,C., Wang,Y., Watanabe,Y.,
 Wells,C., Wilming,L.G., Wyshaw-Boris,A., Yanagisawa,M., Yang,I.,
 Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
 Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
 Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
 Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
 Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
 Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
 Rogers,J., Birney,E. and Hayashizaki,Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-575 (2002)

RESULT 10
 BY300950
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

22354683
 12466851
 MEDLINE
 PUBMED
 COMMENT
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.go.jp/
 URL: http://genome.gsc.riken.go.jp/
 Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
 Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
 Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
 Ono,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
 Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
 Hayashizaki,Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Michelle Brinkmeier and Sally Camper (Dept.
 Human Genetics University of Michigan Medical School 4301
 MSRB 3 1500 W. Medical Center Dr. Ann Arbor, MI 48109-0638 USA)
 whose assistance we gratefully acknowledge.
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.

Location/Qualifiers
 1. 372
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="K720012M21"
 /tissue_type="Rathke's pouches"
 /dev_stage="14.5 days embryo RP/+"
 /clone_lib="RIKEN full-length enriched, 14.5 days embryo
 RP/+ Rathke's pouches"

Query Match 2.2%; Score 78.8; DB 13; Length 372;
 Best Local Similarity 69.5%; Pred. No. 2.8e-07;
 Matches 107; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1307 GCCTGGAGCCCTCATCTCCAGGAGATCATGACCTTACACACAGCACCATCAG 1366
 Db 7 GCGCTGGAGCCACATTAACGCGCAGATCATGCGCTGCACCAAGCACCATGCG 66
 QY 1367 ACTTATGTTAAACGGCTCAACGGTGGCGGAGAGTACTCGGCGGTGGGCAAGGAG 1426
 Db 67 GCGTACGTGAACACCTCAACGCCACGAGGAGAGTACACAGGCTCTGGCCAAAGGA 126
 QY 1427 GATGTGTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
 Db 127 GATGTTACAACCTCAGGTGCGCTCTTCAGCTGCAC 160

RESULT 11
 CB274248
 LOCUS
 DEFINITION
 CB274248
 467 bp mRNA linear EST 24-FEB-2003
 ma190f09.yl McCarrey Eddy round spermatid Mus musculus cDNA clone
 IMAGE:6448769 5' similar to SW:SODM_MOUSE P09671 SUPEROXIDE

DISMUTASE [MN], MITOCHONDRIAL PRECURSOR ;, mRNA sequence.

CB274248
CB274248.1 GI:28464571

EST.
Mus musculus (house mouse)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 467)
McCarrey, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Pape, D.,
Martin, J., Wylie, T., Dente, M., Bowers, Y., Theising, B., Gibbons, M.,
Ritter, E., Tsagaris, V., Ronko, I., Maguire, L., Kennedy, S.,
Bennett, J., Waterston, R. and Wilson, R.

NIEHS Mouse
Unpublished (2002)
Contact: McCarrey/Eddy NIEHS Mouse
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed and donated by J. McCarrey, Ph.D. (Southwest
Foundation for Biomedical Research, Dept. of Genetics) - excision
done by E.M. Eddy, Ph.D. (National Institutes of Health, National
Institute of Environmental Health Sciences).

MG1:2072729
Seq primer: Primer name ambiguous
High quality sequence stop: 427.

FEATURES
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/dev_stage="60 day"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pBluescript SK+
Stratagene); Site 1: XhoI; Site 2: EcoRI; cDNA oligo
directionally cloned using 5' linkers 5'-AATTCGCGACGAG-3'
and 5'-CTCGGCGC-3'. Size selection of >400bp material
gives average insert size ranging from 1-2 kb. Library was
mass excised (from lambda-UniZAP-XR) and retransformed
single-stranded phagemids were prepped and transformed
into DH10B. Library contains 98.5% recombinants.
References: J. Androl. 20:635-639 and Gene 25:263-269.
Library constructed and donated by J. McCarrey, Ph.D.
(Southwest Foundation for Biomedical Research, Dept. of
Genetics); excision done by E.M. Eddy, Ph.D. (National
Institutes of Health, National Institute of Environmental
Health Sciences). Original lambda-based library is
available through ATCC, catalog #63423."

RESULT 13
CA889637
LOCUS
DEFINITION
B0154B09-5N NTA Mouse Neural Stem Cell (Differentiated) cDNA
Library (Long) Mus musculus cDNA clone NTA:B0154B09 IMAGE:30098996
5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 566)
Piao, Y., Dudekula, D.B., Qian, Y., Martin, P.R., Aiba, K., Vescovi, A.L.
and Ko, M.S.H.
Systematic Analyses of NTA Mouse Neural Stem Cell (Differentiated)

10273-74 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.

FEATURES
Location/Qualifiers
1..511
/organism="Mus musculus"
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Matches 107; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1307 GCCTGGAGCCCTCCATCTCCAGGAGATCATGACCTTCACACACAGCAGCATCAG 1366
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QY 1367 ACTTATGTTAAGCGCTCAACGCTCCGAGGAGAGTACTCGCGCGCTGTGGCAAGGAG 1426
Db 274 GCCTAGTGAAACACCTCAACGCCACCGAGGAGAGTACCAGAGGCTCTGCCAAGGGA 333
QY 1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
Db 334 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 367

Query Match 2.2%; Score 78.8; DB 14; Length 467;
Best Local Similarity 69.5%; Pred. No. 2.8e-07;
Matches 107; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1307 GCCTGGAGCCCTCCATCTCCAGGAGATCATGACCTTCACACACAGCAGCATCAG 1366
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JOURNAL COMMENT

CDNA Library (Long)
Unpublished (2002)
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@ngun.grc.nia.nih.gov
Plate: B0154 row: B column: 09
Seq primer: -21M13 Reverse
High quality sequence stop: 566
POLYA-No.

FEATURES

source

Location/Qualifiers

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/clone_lib="NIA Mouse Neural Stem Cell (Differentiated)
CDNA Library (Long)"
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NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://igun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001)). [PMID: 11544199]. Total RNAs were
obtained from Dr. Angelo L. Vescovi (Institute for Stem
Cell Research, Italy). Double-stranded cDNAs were
synthesized with an Oligo(dT) primer [Invitrogen:
5'-pGACTAGTCTAGATCGGAGCGCGCTTTTCTTTT-3'] from
2.0 Microgram of total RNA, treated with T4 DNA
polymerase, and purified by ethanol-precipitation. The
cDNAs were ligated to lone-linker LL-Sal4, purified by
phenol/chloroform, and separated from free linkers by
Centricon 100. Then, the cDNAs were amplified by
long-range high fidelity PCR using Ex-Taq polymerase
(Takara) with a primer Sal4-S. The products were purified
by phenol/chloroform and Centricon 100. The cDNAs were
digested with SalI and NotI enzymes and cloned into
SalI/NotI site of pSPORT1 plasmid vector. The DH10B E.
coli host was transformed with the ligation mixture by the
standard chemical method. The average insert size is about
3.2 kb. The library was constructed by Yulan Piao."

ORIGIN

Query Match 2.2%; Score 78.8; DB 14; Length 566;
Best Local Similarity 69.5%; Pred. No. 2.8e-07;
Matches 107; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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|||||

QY 1427 GATGTGCTTACCAGGTTAAGCTTCAGTCTGTAC 1460
|||||

Db 323 GATGTTACAACACTCAGTCTGCTCTTCAGCTGCGAC 356
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musculus cDNA clone IMAGE:5660725 5' similar to SW:SDM MOUSE
P09671 SUPEROXIDE DISMUTASE [NM], MITOCHONDRIAL PRECURSOR i, mRNA
sequence.
BI713308
ACCESSION

BI713308.1 GI:15689003
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 580)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Elistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R.,
Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: ic86g07.xl
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
MGI:1947051 This sequence now available from the IMAGE consortium,
for clone orders contact: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 413.
Location/Qualifiers
1. 580
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NI-MMS1"
/note="Vector: pSPORT1; Site 1: Not I; Site 2: Sal I; Five
libraries representing E10.5/12.5 pancreatic bud, E16.5
pancreas, newborn pancreas, adult pancreas, and adult
islets of Langerhans were separately constructed using
Superscript Plasmid Library kit (Life Technologies). cDNA
was made by oligo-dT priming and size-selected by column
fractionation. Libraries were amplified once on solid
support and plasmid DNA from each library was prepared
and mixed in equal amounts. The mixed library DNA was
normalized by method #4 from Bonaldo, Lennon, and Soares
1996 Genome Research 6:791-806; 0.5 microgram
single-stranded mixed library plasmid DNA was mixed with
5 micrograms PCR product representing mixed library
inserts and hybridized to an EcoT of 6. Single-stranded
(unhybridized) plasmids were isolated by hydroxyapatite
chromatography and used to make this library."

ORIGIN

Query Match 2.2%; Score 78.8; DB 12; Length 580;
Best Local Similarity 69.5%; Pred. No. 2.8e-07;
Matches 107; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1307 GCCTGGAGCCCTCCATCTCCAGGAGATCATGACCTTCACACCAAGCACCATCAG 1366
|||||
Db 110 GCGCTGGAGCCACATTAACGGCAGATCATGCGCTGCACACCAAGCACCATGCG 169
|||||

QY 1367 ACTTATGTTAAACGGCTCAACGCTGCCGAGGAGAGTACTCGCGCTCTGGCGAGGAG 1426
|||||

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QY

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Db

1367 ACTTATGTAAACGGCTCAACGTCGCCGAGGAGAGTACTCGGCCGCTCTGGGCAAGGAG 1426
QY

182 GCTTAGTGAAACAACCTCAACGCCACCGAGGAGAGTACCACGAGGCTCTGGCCAAAGGA 241
Db

1427 GATGTCTCTTACCAGGTTTAAGCTTCAAGTCTGTAC 1460
QY

242 GATGTTACAACTCAGTCGCTCTTTCAGCCTGCAC 275
Db

Search completed: April 1, 2004, 21:52:24
Job time : 9345 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 10:57:14 ; Search time 255.87 Seconds
(without alignments)
7877.372 Million cell updates/sec

Title: US-09-727-855B-1

Perfect score: 3632

Sequence: 1 tctgtgtgataatctttcta.....aagagcttggaaccttag 3632

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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- 2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	84.2	2.3	728	4	US-09-091-097-5
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4	74	2.0	813	3	US-09-151-052-1
5	74	2.0	829	4	US-09-023-655-1348
6	74	2.0	1032	6	5240847-25
7	72.4	2.0	594	3	US-09-075-019-1
8	72.4	2.0	581	3	US-09-075-019-6
9	72.4	2.0	369	2	US-08-365-486A-27
10	72.4	2.0	969	3	US-08-880-342-27
11	72.4	2.0	976	3	US-09-126-109-1
12	72.4	2.0	3789	3	US-09-075-019-8
13	71	2.0	3300	2	US-08-928-692-29
14	71	2.0	3300	4	US-09-339-972-29
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16	70.8	1.9	977	4	US-09-091-097-7
17	66.2	1.8	812	4	US-08-486-953A-2
18	65.2	1.8	1143	4	US-09-373-731-1
19	64.4	1.8	600	6	5240847-16
20	63.6	1.8	630	4	US-09-091-097-29
21	62.8	1.7	600	6	5240847-9
22	62.8	1.7	600	6	5240847-17
23	62.8	1.7	987	6	5240847-19
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25	62.4	1.7	623	6	5240847-1
26	61.2	1.7	600	6	5240847-8
27	60	1.7	7218	1	US-08-232-463-14

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28	58	1.6	495	1	US-08-133-711-41	Sequence 41, Appl
29	57.6	1.6	491	1	US-08-133-711-42	Sequence 42, Appl
30	56.8	1.6	621	4	US-09-214-909-23	Sequence 23, Appl
31	55.8	1.5	522	6	5240847-5	Patent No. 5240847
32	52.8	1.5	491	1	US-08-133-711-34	Sequence 34, Appl
33	51.2	1.4	491	1	US-08-133-711-38	Sequence 38, Appl
34	51.2	1.4	491	1	US-08-133-711-39	Sequence 39, Appl
35	50.6	1.4	491	1	US-08-133-711-33	Sequence 33, Appl
36	49.8	1.4	4403765	3	US-09-103-840A-2	Sequence 2, Appl
37	49.8	1.4	4411529	3	US-09-103-840A-1	Sequence 1, Appl
38	49.6	1.4	491	1	US-08-133-711-37	Sequence 37, Appl
39	49	1.3	490	1	US-08-133-711-43	Sequence 43, Appl
40	48.8	1.3	624	4	US-09-252-991A-8022	Sequence 8022, Ap
41	48.8	1.3	705	4	US-09-252-991A-7972	Sequence 7972, Ap
42	48.8	1.3	999	4	US-09-252-991A-8294	Sequence 8294, Ap
43	47.6	1.3	306	4	US-09-091-097-13	Sequence 13, Appl
44	47.6	1.3	427	4	US-09-091-097-41	Sequence 41, Appl
45	47.4	1.3	491	1	US-08-133-711-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: ptz9pt-f1s
US-08-232-463-14

Query Match 2.6%; Score 94.8; DB 1; Length 7218;

NAME/KEY: mat_peptide
LOCATION: 115..708
US-08-927-230A-1

Query Match 2.0%; Score 74; DB 2; Length 813;
Best Local Similarity 67.5%; Pred. No. 2e-12;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1307 GCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCCTTCAACACCAAGCACCATCAG 1366
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Db 151 GCCTGGAACTCATCATCAACGGCGAGATCATGAGCTGCACCAAGCACCACGCG 210
QY 1367 ACTTATGTTAAAGCCCTCAACGCTGCCGAGGAGAGTACTCGGCCGCTGTGGCAAGGAG 1426
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Db 211 GCCTAGCTGAACAACCTGAACGTCACCGAGGAGAGTACCAAGGAGGCTTGGCCAGGGA 270
QY 1427 GATGTGCTTACCAGGTTAAGCTTCACTCTGTATC 1460
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Db 271 GATGTTACAGCCAGATAGCTCTTACGCTGCAC 304

RESULT 4
US-09-151-052-1
; Sequence 1, Application US/09151052
; Patent No. 6107070
; GENERAL INFORMATION:
; APPLICANT: Nick et al.
; TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Floor 24
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/151,052
; APPLICATION NUMBER:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/927,230
; FILING DATE: September 10, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: UFG-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..708
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 115..708
US-09-151-052-1

Query Match 2.0%; Score 74; DB 3; Length 813;
Best Local Similarity 67.5%; Pred. No. 2e-12;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1307 GCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCCTTCAACACCAAGCACCATCAG 1366
|||||
Db 151 GCCTGGAACTCATCATCAACGGCGAGATCATGAGCTGCACCAAGCACCACGCG 210
QY 1367 ACTTATGTTAAAGCCCTCAACGCTGCCGAGGAGAGTACTCGGCCGCTGTGGCAAGGAG 1426
|||||
Db 211 GCCTAGCTGAACAACCTGAACGTCACCGAGGAGAGTACCAAGGAGGCTTGGCCAGGGA 270
QY 1427 GATGTGCTTACCAGGTTAAGCTTCACTCTGTATC 1460
|||||
Db 271 GATGTTACAGCCAGATAGCTCTTACGCTGCAC 304

RESULT 5
US-09-023-655-1348
; Sequence 1348, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1348:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 829 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g34710
US-09-023-655-1348

Query Match 2.0%; Score 74; DB 4; Length 829;
Best Local Similarity 67.5%; Pred. No. 2e-12;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1307 GCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCCTTCAACACCAAGCACCATCAG 1366
|||||
Db 175 GCCTGGAACTCATCATCAACGGCGAGATCATGAGCTGCACCAAGCACCACGCG 234
QY 1367 ACTTATGTTAAAGCCCTCAACGCTGCCGAGGAGAGTACTCGGCCGCTGTGGCAAGGAG 1426
|||||

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Db 235 GCCTAGCTGAACACCTGAAGCTCACCGAGGAGATACCGAGGCGGTTGGCCAAAGGA 294
Qy 1427 GATGTGTTACCGAGGTTAAGCTTCACTGCTGTAC 1460
Db 295 GATGTACGCCAGATAGCTCTTCAGCCTGCAC 328

RESULT 6
5240847-25
; Patent No. 5240847
; APPLICANT: HECKL, KONRAD; SPEVAK, WALTER; OSTERMANN, ERLINBORG;
; ZOPHEL, ANDREAS; KRYSTEK, EDELTRAUD; MAURER-FOGY, INGRID;
; WICHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
; TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
; (HWN-SOD)
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/167,261
; FILING DATE: 11-MAR-1988
; SEQ ID NO:25:
; LENGTH: 1032
5240847-25

Query Match 2.0%; Score 74; DB 6; Length 1032;
Best Local Similarity 67.5%; Pred. No. 2.4e-12;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 1307 GCCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCCTTACCACCAAGCACCATCAG 1366
Db 109 GCCCTGGAACTCATACACGCGGAGATCATGAGCTGCGACCAAGCAACGCG 168
Qy 1367 ACTTATGTTAAGCGCTCAAGCTGCCGAGAGAGTACTCGGCCGTGTGGCAAGGAG 1426
Db 169 GCCTACGTGAACACCTGAAGCTACCGAGGAGTACCGAGGCGGCTTGGCCAAAGGA 228
Qy 1427 GATGTGTTACCCAGTTAAGCTTCACTGCTGTAC 1460
Db 229 GATGTACGCCAGATAGCTCTTCAGCCTGCAC 262

RESULT 7
US-09-075-019-1
; Sequence 1, Application US/09075019
; Patent No. 6190658
; GENERAL INFORMATION:
; APPLICANT: UTC IR459
; TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
; TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/075,019
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2848-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 681 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..681
; US-09-075-019-6
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 594 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..594
US-09-075-019-1

Query Match 2.0%; Score 72.4; DB 3; Length 594;
Best Local Similarity 66.9%; Pred. No. 4.9e-12;
Matches 103; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 1307 GCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCCTTACCACCAAGCACCATCAG 1366
Db 37 GCCCTGGAACTCATACCAAGCGGAGATCATGAGCTGACCAAGCAAGCACCACGCG 96
Qy 1367 ACTTATGTTAAGCGCTCAAGCTGCCGAGAGAGTACTCGGCCGTGTGGCAAGGAG 1426
Db 97 GCCTACGTGAACACCTGAAGCTCACCGAGGAGTACCGAGGCGGTTGGCCAAAGGA 156
Qy 1427 GATGTGTTACCCAGTTAAGCTTCACTGCTGTAC 1460
Db 157 GATGTACGCCAGATAGCTCTTCAGCCTGCAC 190

RESULT 8
US-09-075-019-6
; Sequence 6, Application US/09075019
; Patent No. 6190658
; GENERAL INFORMATION:
; APPLICANT: UTC IR459
; TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
; TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/075,019
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2848-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 681 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..681
; US-09-075-019-6

Query Match 2.0%; Score 72.4; DB 3; Length 681;
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Best Local Similarity 66.9%; Pred. No. 5.5e-12;
Matches 103; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1307 GCCCTGGAGCCCTCCATCTCCAAAGGAGATCATGCCCTTCCACACCAAGCACCATCAG 1366
Db 43 GCCCTGGAACTCATCAACGGCGAGATCATGCGCTGCACCAAGCACCACGCG 102

QY 1367 ACTTATGTTAAAGCCCTCAACGCTGCCGAGGAGAGCTACTCGGCGCTGTGGGAAGGAG 1426
Db 103 GCCTACGTGAACAACCTTGAACGTCACCGAGGAGAGTACCAAGGCGTGGCCAAAGGA 162

QY 1427 GATGTGCTTACCCAGGTTAAAGCTTCAGTCTGTAC 1460
Db 163 GATGTTACAGCCAGACAGCTCTTTCAGCCTGCAC 196

RESULT 9
US-08-365-486A-27
; Sequence 27, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 969 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: human manganese superoxide dismutase
; INDIVIDUAL ISOLATE: EMBL #X59445
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 61..729
US-08-365-486A-27

Query Match 2.0%; Score 72.4; DB 2; Length 969;
Best Local Similarity 66.9%; Pred. No. 7.2e-12;
Matches 103; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1307 GCCCTGGAGCCCTCCATCTCCAAAGGAGATCATGCCCTTCCACACCAAGCACCATCAG 1366
Db 169 GCCCTGGAACTCATCAACGGCGAGATCATGCGCTGCACCAAGCACCACGCG 228

QY 1367 ACTTATGTTAAAGCCCTCAACGCTGCCGAGGAGAGCTACTCGGCGCTGTGGGAAGGAG 1426
Db 229 GCCTACGTGAACAACCTTGAACGTCACCGAGGAGAGTACCAAGGCGTGGCCAAAGGA 288

QY 1427 GATGTGCTTACCCAGGTTAAAGCTTCAGTCTGTAC 1460
Db 289 GATGTTACAGCCAGATAGCTCTTTCAGCCTGCAC 322

RESULT 10
US-08-880-342-27
; Sequence 27, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,342
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB95/00996
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/365,486
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 969 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: human manganese superoxide dismutase
; INDIVIDUAL ISOLATE: EMBL #X59445
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 61..729
US-08-880-342-27

Query Match 2.0%; Score 72.4; DB 3; Length 969;
Best Local Similarity 66.9%; Pred. No. 7.2e-12;
Matches 103; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1307 GCCTGGAGCCCTCATCTCCAGGAGATCATGACCTTACACCAAGCACCATCAG 1366
 Db 169 GCCCTGGAACCTCATCAACGCCGAGATCATGAGTGCACACAGCAACACCGCG 228
 QY 1367 ACTTATGTAAAGCGCTCAACGCTGCCGAGGAGAGTACTCGCGCGTGTGGGCAAGGAG 1426
 Db 229 GCCTACGTGAACACCTGACGTCACAGGAGAAGTACACGAGGAGCGTGTGGCCAAGGGA 288
 QY 1427 GATGTGTTACCGAGTTAAAGCTTCAGTCTGTAC 1460
 Db 289 GATGTTACAGCCACGATAGCTCTTCAGCCTGCAC 322

RESULT 11
 US-09-126-109-1
 ; Sequence 1, Application US/09126109
 ; Patent No. 6171856
 ; GENERAL INFORMATION:
 ; APPLICANT: Thigpen, Anice
 ; APPLICANT: Hohmeier, Hans-Ewald
 ; APPLICANT: Newgard, Christopher B.
 ; APPLICANT: Unger, Roger H.
 ; APPLICANT: Shimabukuro, Michio
 ; APPLICANT: Chen, Guaxun
 ; APPLICANT: Rhodes, Christopher J.
 ; APPLICANT: Hugl, Sigrun R.
 ; APPLICANT: Cousin, Sharon
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
 ; TITLE OF INVENTION: TO NO-MEDIATED CYTOTOXICITY
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: USA
 ; ZIP: 77210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/126,109
 ; FILING DATE: 30-JUL-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/055,092
 ; FILING DATE: 30-JUL-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US Unknown
 ; FILING DATE: 03-MAR-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McMillian, Nabeela R.
 ; REGISTRATION NUMBER: P-43,363
 ; REFERENCE/DOCKET NUMBER: UTSD:560
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (512) 418-3000
 ; TELEFAX: (512) 474-7577
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 976 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-09-126-109-1

Query Match 2.0%; Score 72.4; DB 3; Length 976;
 Best Local Similarity 66.9%; Pred. No. 7.2e-12;
 Matches 103; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
 QY 1307 GCCTGGAGCCCTCATCTCCAGGAGATCATGACCTTACACCAAGCACCATCAG 1366

Db 203 GCCCTGGAACCTCATCAACGCCGAGATCATGAGTGCACACAGCAACACCGCG 262
 QY 1367 ACTTATGTAAAGCGCTCAACGCTGCCGAGGAGAGTACTCGCGCGTGTGGGCAAGGAG 1426
 Db 263 GCCTACGTGAACACCTGACGTCACCGAGGAGAGTACACGAGGAGCGTGTGGCCAAGGGA 322
 QY 1427 GATGTGTTACCGAGTTAAAGCTTCAGTCTGTAC 1460
 Db 323 GATGTTACAGCCACGAGCTCTTCAGCCTGCAC 356

RESULT 12
 US-09-075-019-8
 ; Sequence 8, Application US/09075019
 ; Patent No. 6190658
 ; GENERAL INFORMATION:
 ; APPLICANT: UTC IR459
 ; TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
 ; TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sheridan Ross P.C.
 ; STREET: 1700 Lincoln St., Suite 3500
 ; CITY: Denver
 ; STATE: CO
 ; COUNTRY: USA
 ; ZIP: 80203
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/075,019
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kovarik, Joseph E.
 ; REGISTRATION NUMBER: 33,005
 ; REFERENCE/DOCKET NUMBER: 2848-22
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (303) 863-9700
 ; TELEFAX: (303) 863-0223
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3789 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-09-075-019-8

Query Match 2.0%; Score 72.4; DB 3; Length 3789;
 Best Local Similarity 66.9%; Pred. No. 2e-11;
 Matches 103; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
 QY 1307 GCCTGGAGCCCTCATCTCCAGGAGATCATGACCTTACACCAAGCACCATCAG 1366
 Db 586 GCCCTGGAACCTCATCAACGCCGAGATCATGAGTGCACACAGCAACACCGCG 645
 QY 1367 ACTTATGTAAAGCGCTCAACGCTGCCGAGGAGAGTACTCGCGCGTGTGGGCAAGGAG 1426
 Db 646 GCCTACGTGAACACCTGACGTCACCGAGGAGAAGTACACGAGGAGCGTGTGGCCAAGGGA 705
 QY 1427 GATGTGTTACCGAGTTAAAGCTTCAGTCTGTAC 1460
 Db 706 GATGTTACAGCCACGAGCTCTTCAGCCTGCAC 739

RESULT 13
 US-08-928-692-29
 ; Sequence 29, Application US/08928692


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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/177001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/723-4123
; TELEFAX: 617/723-8962
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 977 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-023-980B-2

Query Match      1.9%; Score 70.8; DB 2; Length 977;
Best Local Similarity 66.2%; Pred. No. 2.3e-11;
Matches 102; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1307 GCCCTGGAGCCCTCCATCTCCAAAGGAGATATGACCCCTTACCAACCAAGCACCATCAG 1366
Db 204 GCCCTGGAACTCTACATCAACGCGCAGATCATGCGCTGCACACAGCAAGCACCCGCG 263
QY 1367 ACTTATGTTAAGCGCTCAACGCTGCCGAGGAGAGTACTCGCGCGCTGTGGGCAAGGAG 1426
Db 264 GCCTACGTGAACAACCTGAACCTACCGAGGAGAGTACCAAGAGGCGGTGGCAAGGGA 323
QY 1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
Db 324 GATGTTACAGCCACAGACGCTCTTCAGCCTGCAC 357

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Search completed: April 1, 2004, 13:45:30
Job time : 266.87 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 10:57:14 ; Search time 47.1302 Seconds
(without alignments)
7877.372 Million cell updates/sec

Title: US-09-727-855B-4

Perfect score: 669

Sequence: 1 atgtctgttcgagcatccct.....gattgcaggctgctctctaa 669

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCITUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	252	37.7	728	4	US-09-091-097-5
2	250.6	37.5	812	4	US-09-091-097-7
3	220.6	33.0	630	4	US-09-091-097-29
4	199.4	29.8	813	2	US-08-927-230A-1
5	199.4	29.8	813	3	US-09-151-052-1
6	199.4	29.8	829	4	US-09-023-655-1348
7	197.8	29.6	1032	6	5240847-25
8	196.2	29.3	969	2	US-08-365-486A-27
9	196.2	29.3	969	3	US-08-880-342-27
10	196.2	29.3	976	3	US-09-126-109-1
11	194.6	29.1	977	2	US-08-023-980B-2
12	194.6	29.1	977	2	US-08-486-953A-2
13	194.4	29.1	3789	3	US-09-075-019-8
14	194	29.0	594	3	US-09-075-019-1
15	194	29.0	681	3	US-09-075-019-6
16	184.4	27.6	600	6	5240847-16
17	182.8	27.3	600	6	5240847-9
18	182.8	27.3	600	6	5240847-17
19	182.8	27.3	987	6	5240847-19
20	181.2	27.1	600	6	5240847-8
21	165.6	24.8	535	6	5240847-6
22	165.6	24.8	623	6	5240847-1
23	157.4	23.5	522	6	5240847-5
24	155.8	23.3	3300	2	US-08-928-692-29
25	155.8	23.3	3300	4	US-09-339-972-29
26	154	23.0	621	4	US-09-214-909-23
27	142	21.2	371	4	US-09-091-097-25

28 139.2 20.8 4403765 3 US-09-103-840A-2
29 139.2 20.8 4411529 3 US-09-103-840A-1
30 139 20.8 1143 4 US-09-373-731-1
31 134.6 20.1 1230025 4 US-09-198-452A-1
32 123.8 18.5 491 1 US-08-133-711-44
33 121.8 18.2 654 4 US-09-489-039A-5056
34 121.8 18.2 702 4 US-09-489-039A-4999
35 121.6 18.2 491 1 US-08-133-711-40
36 119.6 17.9 624 4 US-09-252-991A-8022
37 119.6 17.9 999 4 US-08-252-991A-8022
38 117.4 17.5 491 1 US-08-133-711-36
39 115.8 17.3 491 1 US-08-133-711-37
40 114.2 17.1 491 1 US-08-133-711-34
41 112 16.7 491 1 US-08-133-711-32
42 111.4 16.7 721 4 US-09-262-856A-8
43 111 16.6 491 1 US-08-133-711-38
44 111 16.6 491 1 US-08-133-711-39
45 110.4 16.5 491 1 US-08-133-711-33

ALIGNMENTS

RESULT 1
US-09-091-097-5
; Sequence 5, Application US/09091097
; Patent No. 6432407
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH
; APPLICANT: OKADO, TAKASHI
; APPLICANT: YAGIHARA, TOMOKO
; APPLICANT: KURODA, MASANOBU
; APPLICANT: ONISHI, YOSHIMI
; APPLICANT: KATO, IKUNOSHIN
; APPLICANT: AKIYAMA, KAZUO
; APPLICANT: YASUEDA, HIROSHI
; APPLICANT: YAMAGUCHI, HIDEYO
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
; TITLE OF INVENTION: MALASSEZIA
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/091,097
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0346P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 728 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..618

Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 44, Appli
Sequence 5056, Ap
Sequence 4999, Ap
Sequence 40, Appli
Sequence 8022, Ap
Sequence 8294, Ap
Sequence 36, Appli
Sequence 37, Appli
Sequence 34, Appli
Sequence 32, Appli
Sequence 8, Appli
Sequence 38, Appli
Sequence 39, Appli
Sequence 33, Appli

US-09-091-097-5

Query Match 37.7%; Score 252; DB 4; Length 728;
Best Local Similarity 65.5%; Pred. No. 5e-68;
Matches 385; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

QY 68 TCAGGGAAGACATACCTGCTGAGTTCCTTACGCTTACGATGCGCTGAGCCCTCCA 127
DB 8 TCATGACTGATGACACTCTCCCTCCTCTGCGCTACGCTAGATGCGCTGAGCGCTTTA 67

QY 128 TCTCAAGGAGATCATGACCCCTTCAACACACCAAGCACCACATGACTTATGTTAACGCC 187
DB 68 TCCTTAAGGAGATCATGAGGTTCAACACACCAAGCACCACATGACTTATGTTAACGCC 127

QY 188 TCAACGCTGCGAGGAGAGTACTGCGCGCTGTGGGCAAGGAGATGCTTACCCAGG 247
DB 128 TCAACGCGCGGAGAGGAGTACTGCGCGCTGTGGGCAAGGAGATGCTTACCCAGG 187

QY 248 TTAAGCTTCAGTCTGCTCAAGTTCAACGAGGAGGACACATCAATCACTCTCTGTCT 307
DB 188 TCCAGCTGCAGAGTGGATCAAGTTCAACGCGGTGGCCACATCAACCACTCGCTGTCT 247

QY 308 GGAAGAACTTGGCTCCCTATGATCCGAGGAGGCTACCTCTCTGAAGGACCTCTCAAGA 367
DB 248 GGAAGAACTTGGCTCCCTATGATCCGAGGAGGCTACCTCTCTGAAGGACCTCTCAAGC 307

QY 368 AGGCTATCGAGGAATCTTTTGGTCTTTCGAGGCGCTTCAAGAGAGTTCAACGCTGACA 427
DB 308 AGGCATCGAGCAGGAGTTCGGCGACTTTGAGAAGTTCAAGACGACCTTCAACAGGAGG 367

QY 428 CGCTGTCTTCAAGGATCCGATCGGCTGGCTGGCTTGAACCCGCTTACTAAGAAAGC 487
DB 368 CGGCGGATCCAGGTTTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 424

QY 488 TGAAGTCAACACGACCGCAACACGAGGAGGCTTACTTACTTACTTACTTACTTACTT 547
DB 425 TCGACTGTCTTGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 484

QY 548 TTGACATCTGGAGCAGCTTTTCTACCTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 607
DB 485 GGGATGCTGGAGCAGCTTGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 544

QY 608 CTGCTGTTGGTTCGCTTATCAACTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 655
DB 545 AGGCTGTGGTGAACGCTGGTGAACCTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGG 592

RESULT 2

US-09-091-097-7

Sequence 7, Application US/09091097
Patent No. 6432407
GENERAL INFORMATION:
APPLICANT: TAKESAKO, KAZUO
APPLICANT: OKADO, TAKASHI
APPLICANT: YAGIHARA, TOMOKO
APPLICANT: KURODA, MASANOBU
APPLICANT: ONISHI, YOSHIMI
APPLICANT: KATO, IKUNOSHIN
APPLICANT: AKIYAMA, KAZUO
APPLICANT: YASUEDA, HIROSHI
APPLICANT: YAMAGUCHI, HIDEYO
TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
TITLE OF INVENTION: MALASSEZIA
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESS: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,097
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422-0346P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 2..673
US-09-091-097-7

Query Match 37.5%; Score 250.6; DB 4; Length 812;
Best Local Similarity 63.9%; Pred. No. 1.4e-67;
Matches 379; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

QY 74 CAAAGCATACCTGCTGAGTTCCTTACGCTTACGATGCGCTGAGGAGGAGGAGGAGGAGG 133
DB 72 CCAAGTACACGCTGCGCGCTGCGTACGACTACGCGCGCTGAGCGGCGATCTCGG 131

QY 134 AGGAGATCATGACCCCTTCAACACCAAGCACCACATGACTTATCTTAAGCGCTCAACG 193
DB 132 GCGAGATCATGAGAGCGCACTACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 191

QY 194 CTGCGGAGGAGGAGTACTCTGCGCGCTGTGGGCAAGGAGGAGGAGGAGGAGGAGGAGG 253
DB 192 CGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 251

QY 254 TTGAGTCTGCTTCAAGTTCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 313
DB 252 AGCTGAACGCGATCAAGTTCAACGCGGCTGGCGGAGGAGGAGGAGGAGGAGGAGGAGG 311

QY 314 ACTTGGCTCCCTATGATCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 373
DB 312 ACCTCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 371

QY 374 TCGAGGAGTCTTTTGGTCTTTTCGAGGCGCTTCAAGAGAGGAGGAGGAGGAGGAGGAGG 433
DB 372 TCGACGCGGAGTCTTGGCTCGGCTCGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 431

QY 434 CTGTCGAAGGATCCGAGTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 493
DB 432 GCATCCAGGCGAGCGGCTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 491

QY 494 TCACACGAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 553
DB 492 TCATACGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 551

QY 554 TCTGGGAGCAGCGTTTCTACCTTCTAGTACAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 613
DB 552 CGTGGGAGCAGCGTTTCTACCTTCTAGTACAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 611

QY 614 TTGAGTCCGTTATCAACTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 666
DB 612 TCTGGAGCGTGAATCAACTTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 664

RESULT 3

US-09-091-097-29

```

ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: UFJ-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 43..708
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 115..708
US-08-927-230A-1

Query Match          29.8%; Score 199.4; DB 2; Length 813;
Best Local Similarity 61.8%; Pred. No. 9.2e-52;
Matches 367; Conservative 0; Mismatches 216; Indels 18; Gaps 2;
99 CAGGGCAAAGCATACCGCTGCTTCCTTACGCTTACGATGCCGCTGAGCGCCCTCAT 128

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GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Suan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1348:
SEQUENCE CHARACTERISTICS:
LENGTH: 829 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: G34710
US-09-023-655-1348

Query Match          29.8%; Score 199.4; DB 4; Length 829;
Best Local Similarity 61.1%; Pred. No. 9.2e-52;
Matches 367; Conservative 0; Mismatches 216; Indels 18; Gaps 2;

QY 69 CAGGGCAAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 128
Db 132 CAGGCGAAGCACAGCCTCCCGACCTGCCCTACGACTACGGGCGCTTGAACCTCACAT 191

QY 129 CTCGAAGGAGATCATGACCCCTTCCACACCAAGACCCATCAGACTATGTTTAAAGCCCT 188
Db 192 CAACGCGCAGATCATGAGCTGACACCAAGACCCACGCGCCCTACGTGAACAACT 251

QY 189 CAACGCTGCCGAGGAGAGTACTCGCCCTGTGGGCAAGGAGGATGCTTACCCAGGT 248
Db 252 GAACGTCAACGAGGAGAGTACGAGGAGGCTTGGCCAAAGGAGAGATGTTACAGCCAGAT 311

QY 249 TAAGCTTCACTGCTCTCAAGTTCAACGAGGAGGAGACATCAATCACTCTCTGTTCTG 308
Db 312 AGCTCTTCAGCTGCACTGAAGTTCAATGGTGGTGTATCATATCATATAGCATTTCTG 371

QY 309 GAAGAACTTGGCTCCCTATGAGATCCGAGGAGGCTACCCCTCTCTGAAGGAGCTCTCAAGAA 368
Db 372 GACAAACCTTCAGCCCTAACCGTGGTGGAGAACCA-----AAGGGAGTTGCTGGA 422

QY 369 GCGTATCGAGGATCTTTTGGTCTTTTCGAGGCTTCAAGAGAGTTCACGCTGACAC 428
Db 423 AGCCATCAAAACGAGTCTTTGGTTCCTTTGACAGTTTAAAGGAGAGCTACGCGCTGCATC 482

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QY 429 CGCTGCTGTCCAAAGGATCCGGATGGGGCTG3CTTGGCTTGAACCCGCTTACTAAGAAGCT 488
Db 483 TGTGTGTGTCCAAAGGCTCAGGTTGGGGTTGGCTTGGTTTCAATAAGCAACGGGACACTT 542

QY 489 GGAAGTCACACGACCGCCAAACAGGACCCCTCTGC-----TTACTCACATTTCTTAT 539
Db 543 ACAAAATTGCTGCTTGTCTCAAAATCAGGATCCACTGCAAGGAGCAACAGGCGCTTATTCAC 602

QY 540 CATCGGAGTTGACATCTGGGAGGACGCTTCTACCTTCAGTACAGAACGCTCAAGCCTGA 599
Db 603 GCTGGGGAATTGATGTGTGGGAGCAGCGTTACTACCTTCAGTATATAAAATGTCAGGCGCTGA 662

QY 600 CTATCTCGCTGCTGTTTGGTCCGTTATCAACTACAAGGAGGAGAGCCCGATTGCGAGG 659
Db 663 TTAATCTAAAGCTATTGGAATGTAATCACTGGGAGATGTAATCAAGATACATATGTC 722

QY 660 T 660
Db 723 T 723

RESULT 7
5240847-25
; Patent No. 5240847
; APPLICANT: HECKL, KONRAD; SPEVAK, WALTER; OSTERMANN, ELINEBORG;
; ZOPHEL, ANDREAS; KRYSTEK, EDELTRAUD; MAURER-FOGY, INGRID;
; WICHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
; TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
; (HMN-SOD)
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/167,261
; FILING DATE: 11-MAR-1988
; SEQ ID NO: 25;
; LENGTH: 1032
5240847-25

Query Match          29.6%; Score 197.8; DB 6; Length 1032;
Best Local Similarity 60.9%; Pred. No. 3.2e-51;
Matches 366; Conservative 0; Mismatches 217; Indels 18; Gaps 2;

QY 69 CAGGGCAAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 128
Db 66 CAGGCGAAGCACAGCCTCCCGACCTGCCCTACGACTACGGGCGCTTGAACCTCACAT 125

QY 129 CTCGAAGGAGATCATGACCCCTTCCACACCAAGACCCATCAGACTATGTTTAAAGCCCT 188
Db 126 CAACGCGCAGATCATGAGCTGACACCAAGACCCACGCGCCCTACGTGAACAACT 185

QY 189 CAACGCTGCCGAGGAGAGTACTCGCCCTGTGGGCAAGGAGGATGCTTACCCAGGT 248
Db 186 GAACGTCAACGAGGAGAGTACGAGGAGGCTTGGCCAAAGGAGAGATGTTACAGCCAGAT 245

QY 249 TAAGCTTCACTGCTCTCAAGTTCAACGAGGAGGAGACATCAATCACTCTCTGTTCTG 308
Db 246 AGCTCTTCAGCTGCACTGAAGTTCAATGGTGGTGTATCATATCATATAGCATTTCTG 305

QY 309 GAAGAACTTGGCTCCCTATGAGATCCGAGGAGGCTACCCCTCTCTGAAGGAGCTCTCAAGAA 368
Db 306 GACAAACCTTCAGCCCTAACCGTGGTGGAGAACCA-----AAGGGAGTTGCTGGA 356

QY 369 GCGTATCGAGGATCTTTTGGTCTTTTCGAGGCTTCAAGAGAGTTCACGCTGACAC 428
Db 357 AGCCATCAAAACGAGTCTTTGGTTCCTTTGACAAAGTTTAAAGGAGAGCTACGCGCTGCATC 416

QY 429 CGCTGCTGTCCAAAGGATCCGGATGGGGCTTGGCTTGAACCCGCTTACTAAGAAGCT 488
Db 417 TGTGTGTGTCCAAAGGCTCAGGTTGGGTTGGCTTGGTTTCAATAAGAAACGGGACACTT 476

QY 489 GGAAGTCACACGACCGCCAAACAGGACCCCTCTGC-----TTACTCACATTTCTTAT 539
Db 477 ACAAAATTGCTGCTTGTCTCAAAATCAGGATCCACTGCAAGGAGCAACAGGCGCTTATTCAC 536

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Qy 540 CATCGGAGTTGACATCTGGGAGCAGCGCTTTCTACCTTCAGTACCAAGAACGTTCAAGCCCTGA 599
 Db 537 GCTGGGATGATGTGTGGGAGCAGCGTTACTTCTCAGTATATAAATGTTCAGCCCTGA 596
 Qy 600 CTATCTCGCTGCTGTTTGGTCCGTTATCAACTCAAGAGGAGCAGAGGCCCGGATTCGAGGC 659
 Db 597 TTAICTAAAGCTATTGTTGAATGTAATCAACTGGGAGAACTGAATCAACTGAAGATACATGGC 656
 Qy 660 T 660
 Db 657 T 657

RESULT 8

US-08-365-486A-27
 ; Sequence 27, Application US/08365486A
 ; Patent No. 5834306
 ; GENERAL INFORMATION:
 ; APPLICANT: Webster, Keith A.
 ; APPLICANT: Bishopric, Nanette H.
 ; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
 ; TITLE OF INVENTION: Therapeutic Constructs
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: 350 Cambridge Avenue, Suite 250
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/365,486A
 ; FILING DATE: 23-DEC-1994
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sholtz, Charles K.
 ; REGISTRATION NUMBER: 38,615
 ; REFERENCE/DOCKET NUMBER: 8255-0018
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 324-0880
 ; TELEFAX: (415) 324-0960
 ; INFORMATION FOR SEQ ID NO: 27:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 969 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: human manganese superoxide dismutase
 ; INDIVIDUAL ISOLATE: EMBL #X59445
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 61..729
 ; US-08-365-486A-27

Query Match 29.3%; Score 196.2; DB 2; Length 969;
 Best Local Similarity 60.7%; Pred. No. 9.7e-51;
 Matches 365; Conservative 0; Mismatches 218; Indels 18; Gaps 2;
 Qy 69 CAGGCAAGCATACCTGCTGAGCTTCTTACGCTTACGATGCCCTGGAGCCCTCCAT 128
 Db 126 CAGGCAAGCAGCAGCTCCCGACTGCCCTACGACTAGCGGCCCTGGAACCTCACAT 185
 Qy 129 CTCCTAAGGAGTATACGCTTCCACCAAGCAGCATCAGACTTATGTTAACGGCT 188

Db 186 CAACGCGAGATCATGAGCTGCACCAAGCAAGCAAGCCGCGCTACGTGAACAACCT 245
 Qy 189 CAACGCTCGGAGAGAGCTACTCGCGCGCTGTGGCAAGAGAGATGTGCTTACCCAGGT 248
 Db 246 GAAGCTCAACGAGAGAGTACAGAGAGCGTGTGGCAAGGAGATGTTACAGCCAGAT 305
 Qy 249 TAAGCTTCAGTCTCTCAAGTTCAACGAGGAGGAGACATCAATCACTCTCTGTTCTG 308
 Db 306 AGCTCTTCAGCCTGCATCTGAAGTTCAATGGTGGTGTGTCATATCAATCATAGCAITTTCTG 365
 Qy 309 GAAGAACTTGGCTCCCTATGGATCCGAGAGGCTACCCCTCTCTGAAGGACCTCTCAAGAA 368
 Db 366 GACAAACCTCAGCCCTAACGGTGTGGAGAACCA-----AAGGGAGTTGCTGA 416
 Qy 369 GGCTATCGAGGAATCTTTTGGTCTTTTCGAGGCGCTTCAAGAAAGAGTTCAACGCTGACAC 428
 Db 417 AGCCATCAACGCTGACITTTGTTCTTTGACAAGTTTAAAGGAGAGAGCTGACGGCTGCATC 476
 Qy 429 CGTGTGCTCAAGGATCCGATCGGCTGGCTTGGCTTGAACCGCTTACTAAGAAGCT 488
 Db 477 TGTGGTGTCCAAAGGCTCAGGTTGGGTTGGCTTGGTTTCAATAAGGAACGGGGACACTT 536
 Qy 489 GGAAGTCAACACGACCGCCCAACAGGACCCCTCTGC-----TTACTCACATTTCCCTAT 539
 Db 537 ACAATTCGCTGCTTGTCCAAATCAGATCCACTGCAAGGAACAACAGGCTTATTCCTACT 596
 Qy 540 CATCGGAGTTGACATCTGGGAGCAGCGTTTCTACCTTCAGTACAAAGAACGTTCAAGCCTGA 599
 Db 597 GCTGGGATTCATGTGTGGAGCAGCGTTTACTACCTTCAGTATAAAAAATGTCAGGCTGA 656
 Qy 600 CTATCTCGCTGCTGTTTGGTCCGTTATCAACTACAGGAGGAGGAGGCGCCGATTCGAGGC 659
 Db 657 TTATCTAAAGCTATTGGAATGTAATCAACTGGGAGAACTGTAAGTGAAGAAATACATGGC 716
 Qy 660 T 660
 Db 717 T 717

RESULT 9

US-08-880-342-27
 ; Sequence 27, Application US/08880342
 ; Patent No. 6218179
 ; GENERAL INFORMATION:
 ; APPLICANT: Webster, Keith A.
 ; APPLICANT: Bishopric, Nanette H.
 ; APPLICANT: Murphy, Brian
 ; APPLICANT: Laderoute, Keith R.
 ; APPLICANT: Green, Christopher J.
 ; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
 ; TITLE OF INVENTION: Therapeutic Constructs
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: 350 Cambridge Avenue, Suite 250
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/880,342
 ; FILING DATE: 23-JUN-1997
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/IB95/00996
 ; FILING DATE: 13-NOV-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/365,486

FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 969 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: human manganese superoxide dismutase
EMBL #X59445
FEATURE:
NAME/KEY: CDS
LOCATION: 61..729
US-08-880-342-27

Query Match 29.3%; Score 196.2; DB 3; Length 969;
Best Local Similarity 60.7%; Pred. No. 9.7e-51;
Matches 365; Conservative 0; Mismatches 218; Indels 18; Gaps 2;

QY 69 CAGGGCAAGCATACCCCTGCTGAGCTTCCTTAGCTTACGATGCCCTGGAGCCCTCCAT 128
Db |||||
QY 129 CTCCAAGGAGATCATGCCCTTACCACACCAAGCACCATCAGACTTATGTTAACGGCCT 188
Db |||||
QY 186 CAACGGCGAGATCATGCAGCTGCACACACGACCAAGCACCGCGCTACGTGAACACCT 245
Db |||||
QY 189 CAACGCTGCCGAGAGAGCTACTCGGCCGTGTGGCAAGGAGATGTCTTACCCAGGT 248
Db |||||
QY 246 GAACGTCAACGAGAGAGTACGAGGAGGCTGTGGCCAGGAGATGTTACAGCCCAT 305
Db |||||
QY 249 TAAGCTTCAGTTCCTCTCAAGTTCAACGGAGAGGACACATCAATCACTCTCTGTTCG 308
Db |||||
QY 306 AGCTCTTACGCTGCACTGAAGTTCAATGTGTGGTGCATATCAATCATAGCATTTCTG 365
Db |||||
QY 309 GAGAACTTGGCTCCCTATGATCCGAGGAGGCTACCTCTCTGAAGGACCTCTCAAGAA 368
Db |||||
QY 366 GACAAACCTCAGCCCTTAACGGTGGTGAGAACCA-----AAGGGAGTTGCTGGA 416
Db |||||
QY 369 GGCTATCGAGGAATCTTTGGTCTTTTCGAGGCTTCAAGAGAGTTCAACGCTGACAC 428
Db |||||
QY 417 AGCAATCAACGCTGACTTTGGTCTTTGACAGTTTAAAGAGAGTACGCGCTGATC 476
Db |||||
QY 429 CGCTGCTGTCACAGATTCGAGATGGGCTGGCTTGGCTTGAACCGCTTACTAAGAGCT 488
Db |||||
QY 477 TGTGGTGTCCAAAGGCTCAGGTTGGGTTGGTGTGTTTCAATAAGCAACGGGACACTT 536
Db |||||
QY 489 GGAAGTCACCAACGCGGACACGAGGACCTCTGC-----TTACTCATTCTAT 539
Db |||||
QY 537 ACAAAATGCTGTGTGTCCTCAATCAGGATCCACTGCAAGGAGCAACACAGGCTTATTCAC 596
Db |||||
QY 540 CATCGGAGTTGACATCTGGGAGCAGCTTTCTACTCTTCAAGAAACGTCAGGCTGA 599
Db |||||
QY 597 GCTGGGATTTGATGTGTGGAGACCGTTACTACTCTTCAATATAAATGTTCAGGCTGA 656
Db |||||
QY 600 CTATCTCGCTGCTGTTGGTCCGTTATCAATCAAGGAGGACGAGGCCGATTCAGGC 659
Db |||||
QY 657 TTAATCAAGCTATTGGAATGTAATCACTGGGAGATGTAATCACTGGGAGATGTAATCACTGGC 716
Db |||||
QY 660 T 660
Db 717 T 717

RESULT 10
US-09-126-109-1
Sequence 1, Application US/09126109
Patent No. 6171856
GENERAL INFORMATION:
APPLICANT: Thigpen, Anice
APPLICANT: Hohmeier, Hans-Ewald
APPLICANT: Newgard, Christopher B.
APPLICANT: Unger, Roger H.
APPLICANT: Shimabukuro, Michio
APPLICANT: Chen, Guaxun
APPLICANT: Rhodes, Christopher J.
APPLICANT: Hugel, Sigrun R.
APPLICANT: Cousin, Sharon
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TO NO-MEDIATED CYTOTOXICITY
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,109
FILING DATE: 30-JUL-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,092
FILING DATE: 30-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US Unknown
FILING DATE: 03-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: McMillian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: UTSD:560
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 976 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-126-109-1

Query Match 29.3%; Score 196.2; DB 3; Length 976;
Best Local Similarity 60.7%; Pred. No. 9.7e-51;
Matches 365; Conservative 0; Mismatches 218; Indels 18; Gaps 2;

QY 69 CAGGGCAAGCATACCCCTGCTGAGCTTCCTTAGCTTACGATGCCCTGGAGCCCTCCAT 128
Db |||||
QY 160 CAGGAGAGCAGAGCTCCCGACTGCTTACGACTAGCGGCTGAACTCAT 219
Db |||||
QY 129 CTCCAAGGAGATCATGCCCTTACCACACCAAGCACCATCAGACTTATGTTAACGGCCT 188
Db |||||
QY 220 CAACGGCGAGATCATGCAGCTGCACACACGACCAAGCACCGCGCTACGTGAACACCT 279
Db |||||
QY 189 CAACGCTGCCGAGAGAGCTACTCGGCCGTGTGGCAAGGAGATGTCTTACCCAGGT 248
Db |||||
QY 280 GAAAGTCACCGAGGAGAGTACCAGGAGGCTGTGGCCAGGGAGATGTTACAGCCGAC 339
Db |||||
QY 249 TAAGCTTCAGTCTCTCTCAAGTTCAAGGAGGAGACATCAATCACTCTCTGTCTG 308
Db |||||

Db 340 AGCTCTTCAGCGCTGACCTGAAGTTCAATGGTGGTGCATATCAATCATAGCATTTTCTG 399
Qy 309 GAAGAACTTGGCTCCCTATGGATCCGAGAGGCTACCTCTCTGAGGACCTCTCAAGAA 368
Db 400 GACAAACCTCAGCCCTAAACGGTGGTGGAGAACCCCA-----AAGGGGAGTTGCTGGA 450
Qy 369 GCCTATCAGGAATCTTTTGGTTCCTTCGAGGCTTCAAGAGAAAGTTCAACGCTGACAC 428
Db 451 AGCCATCAACGCTGACTTTGGTTCCTTTCGACAAAGTTTAAGGAGAGCTCAGCGCTGCATC 510
Qy 429 CGCTGCTGTCGAAGATCCGATGGGCTGGCTTGGCTTGAACCGCTTACTTAAGAAGCT 488
Db 511 TGTGGTGTCCAAGGCTCAGGTGGGTTGGCTTGGTTTCAATAAGAAACGGGGACACTT 570
Qy 489 GGAAGTCAACAGCGCCCAACAGGACCTCTGCTTACT-----CACATTCCTAT 539
Db 571 ACAAAATGCTGCTTGTCCAAATCAGGATCCACTGCAAGAAACACAGGCTTTATTCCTACT 630
Qy 540 CATCGAGTTGACATCTGGGAGCAGCTTCTACCTTCAGTACAAGAACGTCAGGCTGGA 599
Db 631 GCTGGGATGATGTGGGAGCAGCTTACTACCTTCAGTATAAAATGTCAAGGCTGGA 690
Qy 600 CTATCTCGCTGCTGTTTGGTTCGCTTATCAACTACAAGAGGAGGAGGCGGCTTGCAGGC 659
Db 691 TTATCTAAAGCTAATTTGGAATGTAATCAACTGGGAGAGTGAATCACTGAAAGATACATGGC 750
Qy 660 T 660
Db 751 T 751

RESULT 11

US-08-023-980B-2
; Sequence 2, Application US/08023980B
; Patent No. 5843641
; GENERAL INFORMATION:
; APPLICANT: Brown, Robert
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Rosen, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
; TREATMENT AND PREVENTION OF DISEASES OF CELL DEATH
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 585 Commercial Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-1024
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/023,980B
; FILING DATE: 26-FEB-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/177001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/723-4123
; TELEFAX: 617/723-8962
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 977 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: DNA
US-08-023-980B-2
Query Match 29.1%; Score 194.6; DB 2; Length 977;
Best Local Similarity 60.6%; Pred. No. 3e-50;
Matches 364; Conservative 0; Mismatches 219; Indels 18; Gaps 2;
Qy 69 CAGGCAAGCATACCTTCGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 128
Db 161 CAGGCAAGCAGACAGCTCCCGACCTCCCTACGACTACGGCGCCCTGGAACTCAT 220
Qy 129 CTCGAAGAGATCATGACCTTCAACACCAAGCACCATCAGACTTATGTAAAGGCT 188
Db 221 CAACGCGCAGATCATGAGCTGCACACAGCAAGCACCACGCGGCTACGTGAACAACCT 280
Qy 189 CAACGCTCCGAGGAGAGCTACTCGCGCTGTGGCAAGGAGGATGCTTACCCAGT 248
Db 281 GAACCTACCGGAGGAGAGTACGAGGCGCTTGGCAAGGGAGAGTTTACAGCCAGAC 340
Qy 249 TAAAGCTTCAGTCTGCTCTCAAGTTCAACGAGGAGGACACATCAATCACTCTCTGTTCTG 308
Db 341 AGCTCTTCAGCTGACTGAACTTCAATGGTGGTGCATATCAATCATAGCATTTTCTG 400
Qy 309 GAAGAACTTGGCTCCCTATGGATCCGAGGAGGCTACCTCTCTGAGGACCTCTCAAGAA 368
Db 401 GACAAACCTCAGCCCTAAACGGTGGTGGAGAACCCCA-----AAGGGGAGTTGCTGGA 451
Qy 369 GCCTATCAGGAATCTTTTGGTTCCTTCGAGGCTTCAAGAGAAAGTTCAACGCTGACAC 428
Db 452 AGCCATCAACGCTGACTTTGGTTCCTTTCGACAAAGTTTAAGGAGAGCTCAGCGCTGCATC 511
Qy 429 CGCTGCTTCCAAAGATCCGGATCGGATGGGCTGGCTTGAACCGCTTACTTAAGAAGCT 488
Db 512 TGTGGTGTCCAAGGCTCAGGTGGGTTGGCTTGGTTTCAATAAGGAGGAGCTCAGCGCTGCATC 571
Qy 489 GGAAGTCAACAGGAGCGCCCAACGAGGACCTCTGCTTACT-----CACATTCCTAT 539
Db 572 ACAAAATGCTGCTTGTCCAAATCAGGATCCACTGCAAGGAAACACAGGCTTTATTCCTACT 631
Qy 540 CATCGAGTTGACATCTGGGAGCAGCTTCTACCTTCAGTACAAGAACGTCAGGCTGGA 599
Db 632 GCTGGGATGATGTGGGAGCAGCTTACTACCTTCAGTATAAAATGTCAAGGCTGGA 691
Qy 600 CTATCTCGCTGCTGTTTGGTTCGCTTATCAACTACAAGGAGGAGGCGGCTTGCAGGC 659
Db 692 TTATCTAAAGCTAATTTGGAATGTAATCAACTGGGAGAGTGAATCACTGAAAGATACATGGC 751
Qy 660 T 660
Db 752 T 752

RESULT 12

US-08-486-953A-2
; Sequence 2, Application US/08486953A
; Patent No. 5849290
; GENERAL INFORMATION:
; APPLICANT: Brown, Robert
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Rosen, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
; TREATMENT AND PREVENTION OF DISEASES OF CELL DEATH
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,953A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/204,052
; FILING DATE: 28-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/223002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/428-0200
; TELEFAX: 617/428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 977 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-486-953A-2

Query Match          29.1%; Score 194.6; DB 2; Length 977;
Best Local Similarity 60.6%; Pred. No. 3e-50;
Matches 364; Conservative 0; Mismatches 219; Indels 18; Gaps 2;

QY 69 CAGGGCAAGCATACCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 128
Db 161 CAGCGAAGACAGACTCCCGACCTGCTAGCTAGCGGCCCTGGAACCTCAT 220

QY 129 CTCGAAGGAGATCATGACCCCTTCAACACCAAGCACCATCAGACTTATGTTAAAGCCCT 188
Db 221 CAACGGGCGAGATCATGCGCTGACACACAGACCAACGCGCCCTACGTGAACACCT 280

QY 189 CAACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGGCAAGGAGATGCTTACCCAGGT 248
Db 281 GAACGTCACCGAGGAGAGTACCAGGAGGCGTTGGCAAGGGAGATGTTACAGCCAGAC 340

QY 249 TAAGCTTCAGTCTGCTCTCAAGTTCAACGGAGGAGACATCAATCACTCTCTGTCTG 308
Db 341 AGCTCTTCAGCCTGCATCGAGTTCAATGTGGTGCATATCAATCATAGCATTTCTG 400

QY 309 GAAGAACTTGGCTCCCTATGGATCCGAGGAGGCTACCCCTCTCTGAAGGACCTCTCAAGAA 368
Db 401 GACAAACCTCAGCCCTAACGGTGGTGAGAACCA-----AAGGGGAGTTGCTGGA 451

QY 369 GCGTATCGAGGAATCTTTTGGTCTTTTCGAGGCCCTTCAAGAAAGTTCAACGCTGACAC 428
Db 452 AGCCATCAACAGCTGACTTTGGTTCCTTTGACAAAGTTTAAAGGAGAGCTGACGGCTGCATC 511

QY 429 CGCTGCTGTCCAAAGATCCGATGGGCTGGCTTGGCTTGAACCCGCTTACTAAGAAAGCT 488
Db 512 TGTGGTGTCCAGGCTCAGGTTGGGTTGGCTTGGTTTCAATGAAGACGGGACACTT 571

QY 489 GGAAGTCACCAAGCCGCAACAGGACCTCTGCTTACT-----CACATTCCTAT 539
Db 572 ACAAAATGCTGTGTCAAATCAGGATCCACTGCAAGGAGCAACACAGGCCCTTATTCACAT 631

QY 540 CATCGGAGTTGACATCTGGGAGCAGCTTTTACCTTCAGTACAAAGACGTCAGCCCTGA 599
Db 632 GCTGGGGAATTGATGTGGGAGCAGCTTACTTACTTTCAGTATATAAATGTCAAGGCCCTGA 691

QY 600 CTATCTCGCTGCTTTTGGTCCGTTATCACTACAAGGAGCAGAGCCCGATGTCAGGC 659
Db 692 TTATCTAAAGCTAATTTGGAATGTAATCACTGGGAGAAATGTAATGAAAGATACATGCG 751

QY 660 T 660
Db 752 T 752

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/075,019
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/075,019
; FILING DATE: 28-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2848-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-09-075-019-8

Query Match          29.1%; Score 194.4; DB 3; Length 3789;
Best Local Similarity 60.4%; Pred. No. 6.7e-50;
Matches 365; Conservative 0; Mismatches 221; Indels 18; Gaps 2;

QY 66 GATCAGGGCAAGCATACCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTC 125
Db 540 GAATATGCATAAGCAGACGCTCCCGACCTGCTAGCTAGCGGCCCTGGNACCTCA 599

QY 126 CATCTCAAGGAGATCATGACCCCTTCAACACCAAGCACCATCAGACTTATGTTAAAGG 185
Db 600 CATCAACGCGCAGATCATGCGCTGACACACAGACCAACGCGGCCCTACGTTGAACAA 659

QY 186 CCTCAACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGCAAGGAGATGCTTACCCA 245
Db 660 CCTGAACGCTCACCAGGAGAGAGTACAGGAGGCGTTGGCCCAAGGAGATGTTACAGCCA 719

QY 246 GGTTAAGCTTCAGTCTGCTCTCAAGTTCAACGGAGGAGGACACATCAATCACTCTCTGTT 305
Db 720 GACAGCTCTTCAGCTGCATCGAAGTTCAATGTGGTGGTGCATATCAATCATAGCATTTT 779

QY 306 CTGAAGAACTTGGCTCCCTATCGATCCGAGGAGGCTACCCCTCTCTGAAGAGACCTCTCAA 365
Db 780 CTGACAAACCTCAGCCCTAAACGCTGCTGGTGGAGAACCA-----AAGGGGAGTTGCT 830

QY 366 GAAGGCTATCGAGGAATCTTTTGGTCTTTTCGAGGCCCTTCAAGAAAGAGTTCAACGCTGA 425
Db 831 GGAAGCCATCAAAACGCTGACTTTGCTTTCCTTTGCAAGTTTAAAGGAGAGCTGACGGCTGC 890

QY 426 CACCGCTGCTGTCCAAAGGATCCGAGTCCGCGCTGGCTTGGCTTGAACCCGCTTACTAAGAA 485
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Db 891 ATCTTTGGTGTCCAAAGGCTCAGTTGGGTTGGCTTGGTTCAATAAGGAACGGGGACA 950
QY 486 GCTGGAAGTCCACGACGCGCAACAGGACCCCTCTGCTTACT-----CACATTCC 536
Db 951 CTTACAAATGCTGTTGTCCTCAATCAGATCCACTGCAAGGAACAACAGGCTTATTCC 1010
QY 537 TATCATCGAGTTGACATCTGGGAGCAGGCTTTCTACCTTCAGTACAAGAACGTCAAGCC 596
Db 1011 ACTGCTGGGATTGATGTGGGAGCACGCTTACTACCTTCAGTATAAAAATGTCAAGCC 1070
QY 597 TGACTATCTCGCTGCTGTTGGTTCGCTTATCAACTACAAGAGGAGGAGCCCGATTGCA 656
Db 1071 TGATTATCTAAAAGCTATTGGAATGTATCAACTGGGAGATGTAACTGAAAGATACAT 1130
QY 657 GGCT 660
Db 1131 GGCT 1134

RESULT 14

US-09-075-019-1
; Sequence 1, Application US/09075019
; Patent No. 6190658
; GENERAL INFORMATION:
; APPLICANT: UTC IR459
; TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
; TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/075,019
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2848-22
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 594 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..594
; US-09-075-019-1

Query Match 29.0%; Score 194; DB 3; Length 594;
Best Local Similarity 60.8%; Pred. No. 3.7e-50;
Matches 361; Conservative 0; Mismatches 215; Indels 18; Gaps 2;
QY 76 AAGCATACCTGCTGAGCTTCTTACGTTACGATGCGCTCGAGCCCTCCATCTCCAAAG 135
Db 1 AAGCACAGCCTCCCGACCTGCGCTACGATACGGCGCCCTGGAACCTCACATCAACGCG 60
QY 136 GAGATCATACCTTCCACACACAGCACCACCTATGTTTAAACGGCTTCAACGCT 195

Db 61 CAGATCATGCTCAGCTCACACACAGCAAGCACACGCGGCTACGTGAACAACTGAACGTC 120
QY 196 GCCGAGGAGAGCTACTTCGGCCCTGTGGCAAGGAGGATGTCTTACCCAGGTTAAGCTT 255
Db 121 ACCGAGGAGAGTACACAGAGCGTGTGGCAAGGAGAGATGTTACAGCCCGACAGCTCTT 180
QY 256 CAGTCTGCTCTCAAGTTCAACGGAGGAGGACACATCAATCACTCTCTGTTCGGAAGAAC 315
Db 181 CAGCCTGCACTGAAGTTCAATGGTGGTGTGTCATATCAATCATAGCATTTTCTGGACAAAC 240
QY 316 TTGGCTCCCTATGATCCGAGAGGAGCTACCTCTCTGAAGGAGCTCTCAAGAGGCTATC 375
Db 241 CTCACCCCTAACGGTGGTGGAAACCCA-----AAGGGGAGTGTCTGGAAGCCATC 291
QY 376 GAGGAATCTTTGGTCTTTGAGGCTTCAAGAAAGAGTTCAACGCTCACACCGCTGCT 435
Db 292 AAACGTGACTTGGTTCCTTTGACAAGTTTAAGGAGAGCTCAGCGTGCATCTGTGGT 351
QY 436 GTCCAAGGATCCGATGGGCTGGCTTGGCTTTGAACCCGCTTACTAAGAGGCTGGAAGTC 495
Db 352 GTCCAAGGCTCAGGTTGGGTTGGCTTGGTTTCAATAAGAAACGGGACACTTACAAAT 411
QY 496 ACCACGACGGCAACACGAGCCCTCTGC-----TTACTCATTCTCTATCATCGA 546
Db 412 GCTGCTTGTCCAATCAGGATCCACTGCAAGGAAACAACAGGCTTATTCCTGCTGGGG 471
QY 547 GTTGACATCTGGGAGCAGGCTTCTACCTTCAGTACAAGAACTCAAGCCTGACTATCTC 606
Db 472 ATTGATGTGGGAGCAGGCTTACTACCTCAGTATAAAATGTCAAGCCTGATATCTA 531
QY 607 GCTGCTGTTGGTCCGTTATCAACTACAAGGAGGAGGAGCCCGATTGAGGCT 660
Db 532 AAAGCTATTGGAAATGTAATCAACTGGGAGATGTAACTGAAAGATACATGGCT 585

RESULT 15

US-09-075-019-6
; Sequence 6, Application US/09075019
; Patent No. 6190658
; GENERAL INFORMATION:
; APPLICANT: UTC IR459
; TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
; TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/075,019
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2848-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 681 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..681
US-09-075-019-6

Query Match      29.0%; Score 194; DB 3; Length 681;
Best Local Similarity 60.8%; Pred. No. 3.9e-50;
Matches 361; Conservative 0; Mismatches 215; Indels 18; Gaps 2;

QY 76 AAGCATACCTGCTCAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCATCTCCAAG 135
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
7 AAGCACAGGCTCCCGACCTGCGCTACGACTACGGCGCCCTGGAACTCACATCAACGGCG 66

QY 136 GAGATCATGACCTTCACACACACAGCACCATCAGACTTATGTTAAGGCTTCAAGCT 195
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
67 CAGATCATGAGCTGCACACACAGCACCACCGCGCCCTACGTGAACACCTGAACGTC 126

QY 196 GCGAGGAGAGCTACTCGGCCGCTGTGGGCAAGGAGGATGTGCTTACCCAGGTTAAGCTT 255
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
127 ACCGAGGAGAGTACCAGGAGGCTTGGCCCAAGGGAGATGTACAGCCACAGAGCTCTT 186

QY 256 CAGTCTGCTCTCAAGTTCAACGAGGAGGACACATCAATCACTCTCTGTCTGGAAGAAC 315
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
187 CAGCTTGCACTCAAGTTCAATGCTGTGTGTCATATCAATCATAGCATTTTCTGGACAAAC 246

QY 316 TTGGCTCCCTATGATCCGAGGAGGCTTACCTCTCTGAAGGACCTCTCAAGAGGCTATC 375
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
247 CTCAGCCCTAACGGTGGTGAGAACCA-----AAGGGAGTTGCTGGAAGGCATC 297

QY 376 GAGGAATCTTTTGGTTCTTTCCGAGGCTTCAAGAAGAAGTTCAACGCTGACACCGCTGCT 435
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
298 AAACGTGACTTTGGTTCTTTTGACAAGTTTAAGGAGAGCTGACGCTGCATCTGTGGT 357

QY 436 GTCCAAAGGATCCGATGGGCTGGCTTGAACCCGCTTACTAAGAAGCTGGAAGTC 495
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
358 GTCCAAAGGCTCAGGTTGGGCTGGCTTGGTTTCAATAAGGAACGGGACACTTACAAATT 417

QY 496 ACCACGACCGCCACACGAGACCTCTGC-----TTACTCACATTCCTATCATCGGA 546
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
418 GCTGCTGTGCCAATCAGGATCCACTGCAAGGAACACAGGCGCTTATCCACTGCTGGGG 477

QY 547 GTTGACATCTGGGAGCACGCTTTCTACCTTCAGTACAAGAAAGCTCAAGCCCTGACTATCTC 606
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
478 ATTGATGTGTGGGAGCACGCTTACTACCTTCAGTATAAATGTACGCCCTGATTATCTA 537

QY 607 GCTGCTGTTTGGTCCGTTATCAACTACAAGGAGGACAGGCCCGGATTCAGGCT 660
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
538 AAAGCTATTGGAATGTAATCAACTGGGAGATGTAACCTGAAAGATACATGGCT 591

```

Search completed: April 1, 2004, 13:45:43
Job time : 60.1302 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 08:33:07 ; Search time 257.583 Seconds
(without alignments)
11033.514 Million cell updates/sec

Title: US-09-727-855B-4

Perfect score: 669

Sequence: 1 atgtctgttcagcatccct.....gattgcaggctgctctctaa 669

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	252	37.7	728	2 AAT85876	Aat85876 Malassezi
2	250.6	37.5	812	2 AAT85877	Aat85877 Malassezi
3	220.6	33.0	630	2 AAT85894	Aat85894 Malassezi
4	211.4	31.6	897	9 ADDJ5245	AdJ5245 Mouse mit
5	205	30.6	1492	6 ABK63720	Abk63720 Rat seque
6	205	30.6	1492	9 ADB58236	Adb58236 Toxicity-
7	203.4	30.4	1438	3 AA75734	Aa75734 Nucleotid
8	199.4	29.8	813	1 AAN81158	Aan81158 cDNA enco
9	199.4	29.8	813	2 AAT853193	Aat853193 MnSOD cDN
10	199.4	29.8	813	2 AAT15589	Aat15589 Human man
11	199.4	29.8	813	2 AAT34277	Aat34277 Human man
12	199.4	29.8	813	2 AAX24998	Aax24998 Human nat
13	199.4	29.8	813	3 AAA63891	Aaa63891 cDNA enco
14	197.8	29.6	813	1 AAN71370	Aan71370 Sequence
15	197.8	29.6	849	6 AAN84891	Aan84891 Human man
16	197.8	29.6	849	6 ABA94453	Aba94453 Human man
17	197.8	29.6	972	7 ABX63836	Abx63836 Human cDN
18	197.8	29.6	1026	6 ABL66512	AbL66512 Lung canc
19	197.8	29.6	1026	6 ABK84524	Abk84524 Human cDN
20	197.8	29.6	1046	2 AAQ94284	Aaq94284 Human man
21	197.8	29.6	2504	4 AAL26545	Aal26545 Human bre
22	196.2	29.3	969	2 AAT31018	Aat31018 Human man
23	196.2	29.3	976	2 AAQ67474	Aaq67474 Human man

ALIGNMENTS

RESULT 1

AAT85876
ID AAT85876 standard; cDNA to mRNA; 728 BP.

AC AAT85876;

XX 27-AUG-2003 (revised)

DT 23-FEB-1998 (first entry)

XX Malassezia fungus MF-3 antigenic protein encoding cDNA.

XX Malassezia; fungus; antigenic; human; IgE; immunoglobulin E; antibody;

KW allergy; antigen; ds.

OS Malassezia.

PH Key Location/Qualifiers

FT CDS 4..621

FT /*tag= a

FT /product= "MF-3_antigenic_protein"

XX WO9721817-A1.

PD 19-JUN-1997.

XX 10-DEC-1996; 96WO-JP003602.

XX 12-DEC-1995; 95JP-00346627.

PR 05-SEP-1996; 96JP-00257612.

PR 05-SEP-1996; 96JP-00257613.

XX (TAKI) TAKARA SHUZO CO LTD.

XX Takesako K, Okado T, Yagihara T, Kuroda M, Onishi Y, Kato I;

PI Akiyama K, Yasueda H, Yamaguchi H;

XX WPI; 1997-332788/30.

XX P-PSDB; AAW29770.

XX Antigenic proteins from the fungus Malassezia - bind to IgE antibodies
PT present in patients with Malassezia allergies, useful for diagnosis,
PT treatment and prevention of such conditions.

XX Claim 53; Page 76-77; 162pp; Japanese.

XX The present sequence encodes a specifically claimed antigenic protein

Aax333940 Human HCM
Aax08429 Human man
Abz83721 Toxicology
Aaf14076 Aspergill
Aav45115 A. fumiga
Aav73824 Human SOD
Aaz39782 Plasmid p
Aaz39779 Human man
Aaq20194 Mn-SOD (I
Aaq70431 MHS:MnSOD
Aaz39781 Human man
Ade76309 Human BSK
Abt09580 Phase-1 R
Aaq70432 MHS2:MnSO
Abn98977 Arabidops
Aac51219 Arabidops
Aac40144 Arabidops
Ade25718 Human cDN
Aan81224 cDNA of f
Aaq94277 Human man
Abz56304 Aspergill
Aan81225 cDNA of f

Db 552 CTGGGAGACGGTCTTCTACCTCCAGTACAGACGCTCAGGCGGAGCTTCAAGGCGA 611
 QY 614 TTTGGTCCGTTATCACTACAGGAGGAGAGGCGGAGTTCAGGCTGCTC 666
 Db 612 TCTGGACCGTGATCACTTTGAGGAGGCGGAGAGCGTCTCAAGGAGGCGCTC 664

RESULT 3
 AAT85894
 ID AAT85894 standard; cDNA to mRNA; 630 BP.
 AC AAT85894;
 XX 27-AUG-2003 (revised)
 DT 23-FEB-1998 (first entry)
 XX Malassezia fungus MF-4 antigenic protein PCR amplification fragment.
 XX Malassezia; fungus; antigenic; human; IgE; immunoglobulin E; antibody;
 KW allergy; antigen; PCR primer; ds.
 XX Malassezia.
 XX WO9721817-A1.
 XX 19-JUN-1997.
 XX 10-DEC-1996; 96WO-JP003602.
 XX 12-DEC-1995; 95JP-00346627.
 PR 05-SEP-1996; 96JP-00257612.
 PR 05-SEP-1996; 96JP-00257613.
 XX (TAKI) TAKARA SHUZO CO LTD.
 PA Takesako K, Okado T, Yagihara T, Kuroda M, Onishi Y, Kato I;
 PI Akiyama K, Yasueda H, Yamaguchi H;
 XX WPI; 1997-332788/30.
 XX Antigenic proteins from the fungus Malassezia - bind to IgE antibodies
 present in patients with Malassezia allergies, useful for diagnosis,
 treatment and prevention of such conditions.
 XX Example 14; Page 99; 162pp; Japanese.

The present sequence represents a PCR amplification fragment of the MF-4 antigenic protein isolated from the fungus Malassezia. The antigenic peptide can bind to IgE antibodies present in patients with allergic conditions. Antigenic proteins, peptides and nucleic acids from the fungus Malassezia can be used in the diagnosis, treatment and prevention of allergic conditions due to Malassezia organisms (such as M.furfur, M. sympodialis and M.pachydermatitis). (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 630 BP; 156 A; 191 C; 180 G; 101 T; 0 U; 2 Other;
 SQ Query Match 33.0%; Score 220.6; DB 2; Length 630;
 Best Local Similarity 62.5%; Pred. No. 2.1e-56;
 Matches 343; Conservative 0; Mismatches 206; Indels 0; Gaps 0;

QY 118 GAGCCCTCCATCTCCAGGAGATCATGACCCCTTACACACACGAGCACCATCAGACTTAT 177
 Db 1 GAACCTGCTTCTGGGGGAGATAATGGAGACGCACTACGAGAGGAGCACCACCGACCTAC 60
 QY 178 GTTAAGCGCTCAACGCTCCGAGGAGACTACTCGCGCGCTGGGCAAGGAGATGTG 237
 Db 61 GTCAACAACCTGAACCGCGGGAGGACAAGCTGATGACGCGCTCCGCGAGCAGCCCG 120
 QY 238 CTTACCCAGGTTAAGCTTTCAGTCTGCTCTCAAGTTCAACGAGGAGGAGACATCAATCAC 297
 Db 121 CTGGCGAGATTGGCGAGCTGAACCGGATCAANTTCTCGGCGTGGCCACATCACCAC 180

QY 298 TCTGTGTTCTGAAGAACTTGGTCCCTATGATCGAGGAGGCTACCCCTCTCTGAAGGA 357
 Db 181 TCGCTCTTCTGGAAGAACTCTCGCGCGAGCAACAGGGCGGCGGAGCTCGACTCGGCG 240
 QY 358 CTTCTCAAGAAGGCTATCGAGGAATCTTTTGGTCTTTTCGAGGCTTCAAGAAGAGTTTC 417
 Db 241 GAGTGGCGTCCGCGATCGACCGGACTTTGGCTCGGTCGACGCCATGAAGGAGAGTTTC 300
 QY 418 AAGCGTGACACCGCTGCTGTCTCAAGGATCCGATGGGGCTGGCTTGGCTTGAACCGCTT 477
 Db 301 AAGCGCGCGCTCGCGGCGCATCCAGGCTATCGGCTGGGGCTGGCTCGGCGCTGAACCCACG 360
 QY 478 ACTAAGAAGCTGGAAGTCAACAGCAGCGCAACAGGACCCCTCTGCTTACTCATCTTCT 537
 Db 361 ACGGAGAGCTGACATCATCAGCCGCGAACCAGGACCCGCTCTCTGTGCGACAAGCG 420
 QY 538 ATCATCGGAGTTGACATCTGGGAGCAGCGCTTTCTACTCTTCAAGAACGCTCAAGCCT 597
 Db 421 CTGATTGGCATCGATCGGTGGGAGCAGCGTACTACCTGAGTACAAGAACGTCGAAGGCC 480
 QY 598 GACTATCTCGTCTGCTTTGGTCCGTTTCACTCAACTCAAGGAGCAGGCGCGGATTCGAG 657
 Db 481 GACTACTTCAAGGCGATCTGGACCGTGATCAACTTTGAGGAGGCGCGAGAGCGTCTCANG 540
 QY 658 GCTGCTCTC 666
 Db 541 GAGGCGCTC 549

RESULT 4
 ADD35245
 ID ADD35245 standard; DNA; 897 BP.
 XX AC ADD35245;
 XX 15-JAN-2004 (first entry)
 XX Mouse mitochondrial DNA sequence SEQ ID NO:3025.
 DE ds; mouse; array; mitochondrial; hybridisation; energy-metabolism;
 KW mitochondrial disease; oxidative phosphorylation dysfunction;
 KW oxidative stress; apoptosis; aging.
 XX Mus musculus.
 OS WO2003020220-A2.
 PN 13-MAR-2003.
 XX 30-AUG-2002; 2002WO-US027886.
 XX 30-AUG-2001; 2001US-0316323P.
 PR 31-AUG-2001; 2001CA-02356540.
 XX (UYEM-) UNIV EMORY.
 PA Wallace DC, Levy S, Kerstann K, Procaccio V;
 XX WPI; 2003-300821/29.
 XX Array containing probes for genes involved in mitochondrial biology,
 useful for determining mitochondrial biology gene expression profiles for
 use in diagnosing pathologies and identifying biochemical pathways.
 PS Claim 2; SEQ ID NO 3025; 201pp; English.
 XX The invention relates to a novel array comprising at least two isolated
 nucleotide molecules, each molecule having a sequence capable of uniquely
 hybridising to a nucleic acid molecule which is an expression product of
 a gene involved in mitochondrial biology. The array comprises two or more
 isolated nucleic acid molecules or spots, each molecule having a sequence
 chosen from sequence of 994 human probes and 2046 mouse probes. An array

of the invention is useful for determining an expression profile of a mouse or human sample containing nucleic acid, by contacting the array with the sample under conditions allowing selective hybridisation, and measuring hybridisation of nucleic acid in the sample to the array to produce an expression profile. The array is also useful for determining an expression profile of a first labelled sample containing nucleic acid relative to a second, differently labelled sample containing nucleic acid. The second sample is a reference or a standard. An array is useful for determining an expression profile diagnostic of an energy-metabolism-related physiological condition. An array of the invention is useful for determining mitochondrial biology gene expression profiles of organisms, such as human, mice and closely related species, tissue and organs of such organisms, which are useful for determining expression profiles diagnostic of energy metabolism-related physiological conditions, identifying such physiological conditions, identifying biochemical pathways, genes, and mutations involved in such physiological conditions, identifying therapeutic agents useful for preventing and/or treating such physiological conditions, evaluating and/or monitoring the efficacy of such therapies, and creating and identifying animal models of human energy metabolism-related physiological conditions. An array is also useful for defining expression signatures or profiles for mitochondrial diseases, as well as distinguishing clinical disorders that result from oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress, apoptosis and aging. An array of the invention contains probes of genes not previously recognised to participate in mitochondrial biology. The sequences shown in ADD33224-ADD33260 represent murine mitochondrial DNA clones used to make the probes of the invention. Some sequences are not present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 1905, 1906, 2408 and 2643.

Seq Sequence 897 BP; 225 A; 214 C; 247 G; 211 T; 0 U; 0 Other;

Query Match 31.6%; Score 211.4; DB 9; Length 897;
 Best Local Similarity 63.2%; Pred. No. 1.5e-53;
 Matches 367; Conservative 0; Mismatches 196; Indels 18; Gaps 2;

59 CAGGCAAGATACCTGCTGAGCTGCTTACGCTTACGATGCGCTGGAGCCCTCCAT 128
 118 CCGGCACAGCAGCAGCTCCAGAGCTGCTTACGACTATGCGGCTGGAGCCACAT 177
 129 CTCACAGGAGATCATGACCTTCCACACAGCAGCAGCATCATGATTTAAGCGCT 188
 178 TAACGGGAGATCATGAGCTGCACACAGCAGCAGCATGCGCTTACGTGAACAT 237
 189 CAACGCTCCGAGGAGATCATGCGGCTGCTGGGCAAGGAGGATGCTTACCCAGGT 248
 238 CAACGCCACGAGGAGATCATGCGGCTGCTGGGCAAGGAGGATGTTACACTCAGT 297
 249 TAAGCTTCACTGCTCTCAAGTTCACGAGGAGGACATCATCACTCTCTTCTG 308
 298 CGCTCTTCAAGCTGACCTTCAAGTTCATGAGGAGGACATTAATCACTTCTG 357
 309 GAAGAACTTGGCTTCTTCAAGTTCGAGGAGGCTACCTTCTGAGGAGCTTCAAGA 368
 358 GACAACTTGAAGCTTCAAGTTCGAGGAGGCTTCAAGGAGTCTCTGGA 408
 369 GCTATCGAGGAACTTTTGGTCTTTCGAGGCTTCAAGGAGGATTCAGGCTGAC 428
 409 GCTATCAAGCTGACTTGGTCTTTCGAGGAGGATTCAGGAGGATTCAGGCTGAC 468
 429 CGCTCTTCCAGGATCGGATCGGCTTGGCTTGGCTTGAACCGCTTCAAGAGCT 488
 469 TGTGGAGTCCAGGTTTCAAGTTCGAGGCTGGGCTGGCTTCAATAGGAGGAGT 528
 489 GGAAGTCAACAGCAGCGCAACAGGAGCTTCTG-----TTACTCATATCCAT 539
 529 ACAGATTGCTGCTCTTATCAGGAGGATTCAGGAGGATTCAGGAGGATTCAGG 588
 540 CATCGAGTTCAGTTCGAGGAGGATTCAGGAGGATTCAGGAGGATTCAGGAGG 599
 599 GCTGGGATTCAGGTTGAGGAGGATTCAGGAGGATTCAGGAGGATTCAGGAGG 648
 600 CTAATCTGCTGTTTGGTTCGCTTATCACTACAGGAGG 640

Db 649 CTATCTGAAGCTATTGGAATGTAATCACTGGGAGATG 689
 RESULT 5
 ABK63720
 ID ABK63720 standard; cDNA; 1492 BP.
 AC ABK63720;
 DT 18-JUN-2002 (first entry)
 XX
 DE Rat sequence differentially expressed in response to a hepatotoxin #1627.
 KW Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
 KW differential expression; centrilobular necrosis; steatosis.
 OS Rattus norvegicus.
 XX
 PN WO200210453-A2.
 PD 07-FEB-2002.
 XX
 PF 30-JUL-2001; 2001WO-US023872.
 XX
 PR 31-JUL-2000; 2000US-0222040P.
 PR 02-NOV-2000; 2000US-0244880P.
 PR 11-MAY-2001; 2001US-0290029P.
 PR 15-MAY-2001; 2001US-0290645P.
 PR 22-MAY-2001; 2001US-0292336P.
 PR 06-JUN-2001; 2001US-0295798P.
 PR 13-JUN-2001; 2001US-0297457P.
 PR 19-JUN-2001; 2001US-0298884P.
 PR 09-JUL-2001; 2001US-0303459P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Mendrick D, Porter MW, Johnson KR, Castle AL, Elashoff MR;
 XX WPI; 2002-241625/29.
 DR
 XX
 PT Predicting toxic effects of compounds or the progression of these toxic
 PT effects by determining the changes in gene expression in tissues or cells
 PT exposed to the toxin and comparing these to gene expression in unexposed
 PT tissues or cells.
 XX
 PS Claim 1; SEQ ID NO 1627; 239pp; English.
 XX
 CC The invention relates to methods for predicting toxic effects of
 CC compounds or the progression of these toxic effects by determining the
 CC global changes in gene expression in tissues or cells exposed to the
 CC toxin and comparing these to gene expression in unexposed tissues or
 CC cells. Also included are methods of predicting at least one toxic effect
 CC of a compound or progression of a toxic effect, preferably the
 CC hepatotoxicity of a compound, comprising detecting the level of
 CC expression in a tissue or cell sample exposed to the compound of two or
 CC more genes listed in the specification, where differential expression of
 CC the genes is indicative of at least one toxic effect or progression. The
 CC method can also be used to identify an agent which modulates the toxic
 CC response and predict cellular pathways that a compound modulates in a
 CC cell. The methods utilise a set of at least two probes (on a solid
 CC support in kit form), where each of the probes comprises a sequence that
 CC specifically hybridises to a gene listed in the specification, a computer
 CC system comprising a database containing information identifying the
 CC expression level in a tissue or cell sample exposed to a hepatotoxin of a
 CC set of genes comprising at least two genes listed in the specification,
 CC identifying the expression level in a tissue or cell of at least one gene
 CC listed in the specification. The method is useful for elucidating global
 CC changes in gene expression and for identifying toxicity markers in
 CC tissues or cell exposed to a known toxin. The genes may be used as
 CC toxicity markers in drug screening and toxicity assays. The genes and
 CC gene expression information may be used as diagnostic markers for the

Db 545 ACAGATTGCGCGCTGCTTAATCAGGACCCACTGCAAGGAACACACAGGCGTTATTCCACT 604
 QY 540 CATCGGAGTTGACATCTGGGAGCACGCTTCTACCTTCAGTACAAGAACGTCAAGCGTGA 599
 Db 605 GCTGGGATGATGTGTGGGAGCACGCTTACTATCTTCAGTATAAAACGTGACACCTGA 664
 QY 600 CTATCTCGCTGCTGTTTGGTCCGTTATCAACTACAAGGAGG 640
 Db 665 CTATCTGAAAGCCATTGGAAATGTAATCAACTGGGAGATG 705

RESULT 7
 AAA75734
 ID AAA75734 standard; DNA; 1438 BP.
 XX
 AC AAA75734;

DT 22-JAN-2001 (first entry)

DE Nucleotide sequence of a manganese superoxide dismutase (Mn SOD).

XX Adeno-associated virus; catalase; superoxide dismutase; demyelination;
 KW optic nerve; reactive oxygen species; optic neuritis; optic disk edema;
 KW demyelinating disease; allergic encephalomyelitis; multiple sclerosis;
 KW allergic encephalomyelitis; blood brain barrier; ss.

XX Synthetic.

OS WO200054595-A1.

PN 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US006839.

XX 15-MAR-1999; 99US-0124398P.

XX (GUYJ) GUY J.

PA (QIXX/) QI X.

PA (HAUS/) HAUSWIRTH W W.

PI Guy J, Qi X, Hauswirth WW;

XX WPI; 2000-618854/59.

XX Use of recombinant adeno-associated virus composition for treating
 PT demyelinating disorders e.g. multiple sclerosis and allergic
 PT encephalomyelitis, comprises viral constructs expressing catalase or
 PT superoxide dismutase.

XX Disclosure; Page 75-76; 78pp; English.

XX The specification describes the use of a recombinant adeno-associated
 CC virus (rAAV) composition. The rAAV comprises a polynucleotide sequence
 CC encoding a mammalian catalase or superoxide dismutase polypeptide to
 CC reduce demyelination in an optic nerve. The rAAV are useful for
 CC scavenging reactive oxygen species in a mammal suspected of having optic
 CC neuritis, to reduce the effects of demyelinating disease in a mammal and
 CC prophylactically used to suppress blood brain barrier disruption in a
 CC mammal having identified allergic encephalomyelitis. The rAAV composition
 CC is useful for reducing symptoms associated with demyelinating diseases
 CC such as optic neuritis, multiple sclerosis, allergic encephalomyelitis,
 CC where the symptoms associated with these disease include optic disk
 CC edema, increase of optic nerve cell count, disruption of blood brain
 CC barrier integrity, increased levels of hydrogen peroxide and
 CC demyelination of axons. The present sequence is expressed using the rAAV
 CC of the invention

XX SQ Sequence 1438 BP; 371 A; 315 C; 368 G; 384 T; 0 U; 0 Other;

Query Match 30.4%; Score 203.4; DB 3; Length 1438;

Best Local Similarity 62.3%; Pred. No. 5.1e-51;

Matches 362; Conservative 0; Mismatches 201; Indels 18; Gaps 2;

QY 69 CAGGGCAAGCATACCCCTGCTGAGCTTCTTACGCTTACGATGCGCTGAGCGCTCCAT 128
 Db 77 CCGGCACAGACAGAGCTCCCTGAGCTGCTTACGACTATGGCGCTGGAGCGCACAT 136
 QY 129 CTCGAAGAGATGATGACCCCTTCCACACCAAGCAACCATCAGACTTATGTTAAAGGCT 188
 Db 137 TAAACGGCAGATCATGAGCTGCACACAGCAAGCACACCGACCTAGCTGAACAATCT 196
 QY 189 CAACGCTGCGGAGGAGCTACTCGCGCTGTGGCAAGGAGGAGTGTCTTACCAGGT 248
 Db 197 GAACGTACCGAGGAGAGTACACGAGGCGCTGGCCAAAGGAGATGTTACAACTCAGGT 256
 QY 249 TAAGCTTCAGTCTGCTCTCAAGTTCAACGAGGAGGAGACACATCAATCACTCTCTGTTCTG 308
 Db 257 TGTCTTTCAGCTGCACTCAAGTTCAATGCGGGGCGCATATCAATCACAGCATTTTCTG 316
 QY 309 GAAGAACTTGGCTCCCTATGATGATCCGAGGAGGCTACCTCTCTGTAAGGACCTCTCAAGAA 368
 Db 317 GACAAACCTGAGCCCTAAGGCTGGTGGAGAACCCA-----AAGGAGAGTTGCTGGA 367
 QY 369 GGTATCGAGGAATCTTTTGGTTCTTTCGAGGCTTCAAGAGAGTTCAGCGCTGACAC 428
 Db 368 GGTATCAAGCGTGACTTTGGGTCTTTTGAAGAGTTTAAAGGAGAACTGACAGCTGTGC 427
 QY 429 CGCTGCTGCCAAGGATCCGATCGGCTGGGCTTGGCTTGAACCCGCTTACTAAGAAGCT 488
 Db 428 TGTGGAGTCCAAGGTTCAAGGCTGGGCTGGCTTGGCTTCAATAGGAGCAAGGTCGCTT 487
 QY 489 GGAAGTCAACAGCAGCGGCAACAGGACCGCTCTGC-----TTACTCACATTCCTAT 539
 Db 488 ACAGATTGCGCGCTGCTCTAATCAGAACCCACTGCAAGGAAACACACAGGCTTATTCCT 547
 QY 540 CATCGAGTTGACATCTGGGAGCAGCTTTTACCTTCAAGTACAAGAACGTCAGGCTGA 599
 Db 548 GCTGGGATGATGTGTGGGAGCAGCTTACTATCTTTCAGTATATAAAACGTGAGCTGA 607
 QY 600 CTATCTCGCTGCTGTTTGGTCCGTTATCAACTACAAGGAGG 640
 Db 608 CTATCTGAAAGCCATTGGAAATGTAATCAACTGGGAGATG 648

RESULT 8

AA81158

ID AA81158 standard; cDNA; 813 BP.

XX AC AA81158;

XX 22-OCT-1990 (first entry)

XX cDNA encoding human manganese superoxide dismutase.

XX Human manganese superoxide dismutase; ds cDNA; oxygen free radicals.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 43..711

XX FT /*tag= a

XX EP284105-A.

XX 28-SEP-1988.

XX 25-MAR-1988; 88EP-00104880.

XX 27-MAR-1987; 87US-00032734.

XX 26-FEB-1988; 88US-00161117.

XX (BIOT-) BIO-TECHNOLOGY GEN.

XX Hartman JR, Beck Y, Nimrod A;

XX WPI; 1988-272584/39.

DR P-PSDB; AAP80551.
 XX Recombinant human manganese superoxide dismutase - used for treating e.g.
 PT reperfusion injury, inflammation, arthritis, bronchial pulmonary
 PT dysplasia or lung fibrosis.
 XX Disclosure; Page ?; 46pp; English.
 XX The cDNA encodes human manganese superoxide dismutase, and is inserted
 CC into a plasmid, eg pMSE-4 (ATCC 53250)
 XX Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
 SQ

Query Match 29.8%; Score 199.4; DB 1; Length 813;
 Best Local Similarity 61.1%; Pred. No. 6.4e-50;
 Matches 367; Conservative 0; Mismatches 216; Indels 18; Gaps 2;

QY 69 CAGGGCAAGCATACCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 128
 Db 108 CAGGCAAGAGCAGAGCTCCCGACCTGCCCTACGACTACGGCGCCCTGGAACCTCACAT 167
 QY 129 CTCGAAGAGATCATGACCTTCCACACCAAGCAGCAGCTATGTTTAAAGCGCT 188
 Db 168 CAACGGCGAGATCATGAGCTGACACCAAGCAGCAGCTATGTTTAAAGCGCT 227
 QY 189 CAACGCTGCCGAGGAGAGCTACTCGGCCCTGGGCAAGGAGAGTGTCTTACCCAGGT 248
 Db 228 GAACGTCACCGAGGAGAGTACCGAGGAGGCTGGCCCAAGGAGATGTTTACAGCCAGAT 287
 QY 249 TAAGCTTCAGTCTGCTCTCAAGTTCACGAGGAGGACACATCAATCACTCTCTGTCTG 308
 Db 288 AGCTCTTCAGCTGCACTGAAGTTCATGTTGGTGGTTCATATCAATCATAGCATTTTCTG 347
 QY 309 GAAGAACTTGGCTCCCTATGATCCGAGGAGGTACCTCTCTGTAAGAGACCTCTCAGAA 368
 Db 348 GACAAACCTCAGCCCTAACGGTGGTGGAGAACCA-----AAGGGAGTTGCTGGA 398
 QY 369 GGTATCGAGGAATCTTTTGGTCTTTTCGAGGCGCTTCAAGNAGAGTCAACGCTGACAC 428
 Db 399 AGCCATCAACAGTGAAGTGGTGGTTCCTTTGACAAAGTTTAAAGGAGAGTGAAGCTGATC 458
 QY 429 CGCTGCTGTCACAGGATCCGAGTGGGCTGGCTTGGCTTGAACCGCTTACTAAGAGCT 488
 Db 459 TGTGTGTCTCAAGGCTCAGTTGGGTTGGCTTGGTTTCAATGAAGCAACGGGACATTT 518
 QY 489 GGAAGTCACCAACGACCGCCACAGGACCTCTGC-----TTACTCAATTTCTAT 539
 Db 519 ACAATTTGCTGTTGTCCAAATCAGGATCCACTGCAAGGAACACAGGCGCTTATTCACCT 578
 QY 540 CATCGGAGTTGACATCTGGGAGCAGCTTTTACCTTCAGTACAGAACGCTCAAGCCTGA 599
 Db 579 GCTGGGAGTTGATGTGTGGGAGCAGCTTACTTACTTCAGTATAAATGTGAGGCGCTGA 638
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 Db 639 TTATCTAAAGCTATTGGAATGTAATCACTGGGAGAGTGAATGAAGATACATGGC 698
 QY 660 T 660
 Db 699 T 699

RESULT 9

AAQ53193
 ID AAQ53193 standard; cDNA; 813 BP.
 XX
 AC AAQ53193;
 XX
 DT 25-MAR-2003 (revised)
 DT 21-JUN-1994 (first entry)
 XX
 DE MnSOD cDNA.
 XX

MnSOD; manganese superoxide dismutase; N-terminal; catalyze; reperfusion;
 injury; ischaemia; superoxide; SO; molecular oxygen; anti-inflammatory;
 ss.
 Homo sapiens.
 Key Location/Qualifiers
 CDS 43..711
 /tag= a
 /product= "MnSOD"
 US5270195-A.
 14-DEC-1993.
 10-JUL-1992; 92US-00912213.
 22-NOV-1985; 85US-00801090.
 12-SEP-1986; 86US-00907051.
 29-OCT-1986; 86IE-00002851.
 27-MAR-1987; 87US-00032734.
 13-DEC-1989; 89US-00453057.
 (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
 Beck Y, Hartman JR;
 WPI; 1993-404931/50.
 P-PSDB; AAR44801.
 Expression plasmid in Escherichia coli host system - encodes human
 manganese superoxide dismutase analogue, useful for e.g. treating
 inflammation.
 Claim 1; Fig 1a-1c; 27pp; English.
 The sequence encodes a manganese superoxide dismutase which can be used to
 catalyze the reduction of superoxide (SO) radicals to hydrogen peroxide
 and molecular oxygen. It can be used to reduce reperfusion injury
 following ischaemia and prolong the survival of excised organs. It can
 also be used as a long acting anti-inflammatory drug. (Updated on 25-MAR-
 2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
 Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
 Query Match 29.8%; Score 199.4; DB 2; Length 813;
 Best Local Similarity 61.1%; Pred. No. 6.4e-50;
 Matches 367; Conservative 0; Mismatches 216; Indels 18; Gaps 2;

QY 69 CAGGGCAAGCATACCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 128
 Db 108 CAGGCAAGAGCAGAGCTCCCGACCTGCCCTACGACTACGGCGCCCTGGAACCTCACAT 167
 QY 129 CTCGAAGAGATCATGACCTTCCACACCAAGCAGCAGCTATGTTTAAAGCGCT 188
 Db 168 CAACGGCGAGATCATGAGCTGACACCAAGCAGCAGCTATGTTTAAAGCGCT 227
 QY 189 CAACGCTGCCGAGGAGAGCTACTCGGCCCTGGGCAAGGAGAGTGTCTTACCCAGGT 248
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 QY 249 TAAGCTTCAGTCTGCTCTCAAGTTCACGAGGAGGACACATCAATCACTCTCTGTCTG 308
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 Db 348 GACAAACCTCAGCCCTAACGGTGGTGGAGAACCA-----AAGGGAGTTGCTGGA 398
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 Db 399 AGCCATCAACAGTGAAGTGGTGGTTCCTTTGACAAAGTTTAAAGGAGAGTGAAGCTGATC 458

QY 429 CCTGCTGTCCAGGATCCGATGGGCTGGCTTGAACCCGCTTACTAAGAAGCT 488
 Db |||||
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 QY 489 GGAAGTCACACGCGCCCAACGAGACCCCTCTGC-----TTACTCAGATTCCTAT 539
 Db |||||
 QY 519 ACAAAATTGCTGTGTTCCTCAATCAGGATCCCTGCAAGGAACAACAGGCTTATTCCACT 578
 Db |||||
 QY 540 CATCGGAGTTGACATCTGGGACGACGCTTCTACCTTCAGTACAGAACGTCAGCCTGA 599
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 QY 579 GCTGGGATGTGTGTGGAGACGCTTACTACCTTCAGTATATAAATGTCAAGGCTGA 638
 Db |||||
 QY 600 CTATCTCGCTGTGTGTGGTTCGCTTATCACTACAGGAGGAGGCGCCGATTCAGGC 659
 Db |||||
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 QY 660 T 660
 Db 699 T 699

RESULT 10

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ID AAT15589 standard; cDNA; 813 BP.

XX AAT15589;

AC AAT15589;

XX 25-MAR-2003 (revised)

DT 06-APR-1996 (first entry)

XX Human manganese superoxide-dismutase cDNA.

DE Human; manganese superoxide-dismutase; T-lymphocyte; probe; cDNA;

XX Escherichia coli; plasmid pMS8-4; N-terminal truncation; cloning;

KW aminopeptidase; antiinflammatory; oxygen free radical scavenger;

KW synovial inflammation; arthritis; lung fibrosis; GB.

XX Homo sapiens.

OS Key

XX Location/Qualifiers

FH 43..711

FT /tag= a

FT /product= "Manganese superoxide-dismutase"

FT /note= "EC-1.15.1.1"

FT 43..114

FT /tag= b

FT 115..708

FT /tag= c

XX EP691401-A1.

XX 10-JAN-1996.

XX 25-MAR-1988; 95EP-00106995.

XX 27-MAR-1987; 87US-00032734.

XX 26-FEB-1988; 88US-00161117.

XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.

XX Hartman JR, Beck Y, Nimrod A;

XX WPI; 1996-059735/07.

XX P-PSDE; AAR90713.

XX New human manganese superoxide dismutase analogues - having a Lys and

XX opt. His residue absent from the N-terminus, useful for treating e.g.

XX synovial inflammation, arthritis or lung fibrosis.

XX Example 1; Fig 1; 45pp; English.

XX The sequence encodes a human manganese superoxide-dismutase (MnSOD), and

XX has been isolated from a human T-lymphocyte cDNA library in phage lambda-

CC gt10 in Escherichia coli, by screening with a 5'-probe (AAT15591) and a
 CC 3'-probe (AAT15592). The sequence of the insert in plasmid pMS8-4
 CC (obtained by subcloning in plasmid pBR322) is shown. The cDNA may be
 CC expressed in e.g. E. coli for production of recombinant MnSOD. The MnSOD
 CC product may be cleaved with Aeromonas proteolytica aminopeptidase to
 CC produce an N-terminally truncated analogue with lysine and optionally
 CC histidine residues removed. The MnSOD analogue may be used in therapy of
 CC conditions associated with generation of oxygen free radicals,
 CC particularly synovial inflammation, arthritis and lung fibrosis
 CC (claimed). (Updated on 25-MAR-2003 to correct PF field.)
 XX

SQ Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;

Query Match 29.8%; Score 199.4; DB 2; Length 813;

Best Local Similarity 61.1%; Pred. No. 6.4e-50;

Matches 367; Conservative 0; Mismatches 216; Indels 18; Gaps 2;

QY 69 CAGGGCAAGCATACCTGCTGAGCTTCTTACGCTTACGATGCCCTGGAGCCCTCCAT 128
 Db |||||
 QY 108 CAGGCAGGAAGCACAGCCTCCCGACCTGCCCTACGACTAGCGGCCCTGGAACCTCACAT 167
 Db |||||
 QY 129 CTCGAAGGAGATCATGACCTTCACACACAGCAGCACCATCAGACTATGTTAACGGCT 188
 Db |||||
 QY 168 CAACGCGCAGATCATGCGAGCTGCACCCAGCAAGCACCCGCGGCTAGTGAACAACCT 227
 Db |||||
 QY 189 CAACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGCAAGGAGGATGTCTTACCCAGGT 248
 Db |||||
 QY 228 GNACTCACCGAGGAGAGTACCAGAGGCGGTGGCCAGGAGATGTTACAGCCAGAT 287
 Db |||||
 QY 249 TAAGCTTCAGTCTGCTCTCAAGTTCAACGGAGGAGGACACATCAATCACTCTCTGTCTG 308
 Db |||||
 QY 288 AGCTTTCAGCCTGCACCTGAAGTTCAATGGTGTGTCATATCAATCATAGCATTTCTG 347
 Db |||||
 QY 309 GAAGAACTTGGCTCCCTATGATCCGAGAGGCTACCTCTCTGAAGACCTCTCAAGAA 368
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 QY 399 AGCCATCAACGTCAGCTTGGTTCCTTGCAGAGTTTAAGGAGAGCTGACGGCTGCATC 458
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 Db |||||
 QY 459 TGTGGTGTCCAGGCTCAGGTGGGTTGGCTTGGTTTCAATAAGCAACGGGACACTT 518
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 QY 489 GGAAGTCACACGACCGCCCAACGAGGACCTCTGC-----TTACTCAGATTCCTAT 539
 Db |||||
 QY 519 ACAAAATTGCTGTGTTCCTCAATCAGGATCCACTGCAAGGAACAACAGGCTTATTCCACT 578
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 QY 540 CATCGGAGTTGACATCTGGGAGCAGCTTCTTACCTTCAGTACAGAACGTCAGCCCTGA 599
 Db |||||
 QY 579 GCTGGGATGTGTGTGGGAGCAGCTTACTACCTTCAGTATATAAATGTCAAGCCTGA 638
 Db |||||
 QY 600 CTATCTCGCTGTGTGGTCCGTTATCAACTCAAGGAGGAGGAGGCGCCGATTCAGGC 659
 Db |||||
 QY 639 TTATCTAAAGCTATTGGAAATGTAACTCACTGGGAGAAATGTAACCTGAAAGATACATGCG 698
 QY 660 T 660
 Db 699 T 699

RESULT 11

AAT34277

ID AAT34277 standard; cDNA; 813 BP.

XX AAT34277;

AC AAT34277;

XX 25-MAR-2003 (revised)

DT 24-OCT-1996 (first entry)

XX Human manganese superoxide dismutase cDNA.

DE Human; manganese superoxide dismutase; T-lymphocyte; probe; cDNA;

XX Escherichia coli; plasmid pMS8-4; N-terminal truncation; cloning;

KW aminopeptidase; antiinflammatory; oxygen free radical scavenger;

KW synovial inflammation; arthritis; lung fibrosis; GB.

XX Homo sapiens.

OS Key

XX Location/Qualifiers

FH 43..711

FT /tag= a

FT /product= "Manganese superoxide-dismutase"

FT /note= "EC-1.15.1.1"

FT 43..114

FT /tag= b

FT 115..708

FT /tag= c

XX EP691401-A1.

XX 10-JAN-1996.

XX 25-MAR-1988; 95EP-00106995.

XX 27-MAR-1987; 87US-00032734.

XX 26-FEB-1988; 88US-00161117.

XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.

XX Hartman JR, Beck Y, Nimrod A;

XX WPI; 1996-059735/07.

XX P-PSDE; AAR90713.

XX New human manganese superoxide dismutase analogues - having a Lys and

XX opt. His residue absent from the N-terminus, useful for treating e.g.

XX synovial inflammation, arthritis or lung fibrosis.

XX Example 1; Fig 1; 45pp; English.

XX The sequence encodes a human manganese superoxide-dismutase (MnSOD), and

XX has been isolated from a human T-lymphocyte cDNA library in phage lambda-

QY 249 TAAGCTTCAGTCTGCTCAAGTTCAACGAGGAGACATCAATCACTCTCTGTTCTG 308
 Db 288 AGCTCTTCAGCCTGCACCTGAAGTTCAATGGTGGTGCATATCAATCATAGCAATTTCTG 347
 QY 309 GAAGAACTTGGCTCCCTATGATCCGAGGAGGCTACCTCTCTGAAGGACCTCTCAAGAA 368
 Db 348 GACAAACCTCAGCCCTAAACGGTGGTGAGAACCA-----AAGGGAGTTGCTGGA 398
 QY 369 GGTATCGAGGAATCTTTGGTCTTTTCGAGGCTTCAAGAAAGTTCAACGCTGACAC 428
 Db 399 AGCCATCAACGCTGACTTTGGTCCCTTGACAAAGTTTAAAGGAAGCTGACGGCTGCATC 458
 QY 429 CGTGTGCTCCAGGATCCGATGGGCTGGCTTGAACCCGCTTACTAAGAGCT 488
 Db 459 TGTGTGTGTCGAAGGCTCAGTTGGGTTGGCTTGTGTTCAATAAGCAACGGGACACTT 518
 QY 489 GGAAGTCACACACCGCCCAACGAGGACCTCTGC-----TTACTCACATTCCTAT 539
 Db 519 ACAATTCGCTGTGTCCAAATCAGGATCCACTGCAAGGAACACAGGCCCTTATCCACT 578
 QY 540 CATCGAGTTGACATCTGGGAGCAGCTTTCTACCTTCAGTACAAGAACGCTCAAGCTGA 599
 Db 579 GCTGGGATTTGATGTGTGGGAGCAGCTTACTACCTTCAGTATAAAATGTCAAGGCTGA 638
 QY 600 CTATCTCGCTGCTTGTGGTCCGTTTCACTCAACGAGGAGGAGCCCGATTGCGAGG 659
 Db 639 TTATCTAAAGCTATTGGAATGTAATCAACTGGGAGATGTAACTGAAAGATACATGGC 698
 QY 660 T 660
 Db 699 T 699

RESULT 14

AN71370
 ID AAN71370 standard; DNA; 813 BP.

AC AAN71370;

XX 25-MAR-2003 (revised)

DT 10-MAR-2003 (revised)

DT 14-MAY-1991 (first entry)

XX Sequence encoding human manganese superoxide dismutase.

XX Human MSOD; hydrogen peroxide; ischaemia; lesions; inflammation;
 free radicals; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

PH CDS 43..711

FT /*tag= a

FT 115..708

FT /*tag= b

FT /product= "mature MSOD"

XX BE905796-A.

XX 16-MAR-1987.

XX 20-NOV-1986; 86BE-00905796.

XX 22-NOV-1985; 85US-00801051.

XX 22-NOV-1985; 85US-00801090.

XX 12-SEP-1986; 86US-00907051.

XX (BIOT-) BIO-TECHNOL GEN.

XX WPI; 1987-101441/15.

XX P-PSDB; AAN71370.

XX

XX

XX

XX

XX

PT New DNA coding for polypeptide of human manganese superoxidizedismutase -
 useful e.g. for treating inflammation, and new expression vectors and
 transformed cells.

XX Disclosure; Fig 1; 46pp; French.

XX This purified cDNA encodes both prepro- and mature-manganese superoxide
 dismutase (MSOD). It is one strand of a double stranded molecule
 contained in a recombinant vehicle. The MSOD produced catalyses the
 reaction of hydrogen ions and the SOD radical anion to form hydrogen
 peroxide and water. It is useful in veterinary and pharmaceutical
 CC compans. for e.g. reducing lesions of reperfusion following ischaemia, to
 CC prolong survival time isolated organs and for treating inflammation. See
 CC also AAN71371-72. (Updated on 10-MAR-2003 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 813 BP; 218 A; 204 C; 213 G; 178 T; 0 U; 0 Other;

Query Match 29.6%; Score 197.8; DB 1; Length 813;

Best Local Similarity 60.9%; Pred. No. 2e-49;

Matches 366; Conservative 0; Mismatches 217; Indels 18; Gaps 2;

QY 69 CAGGGCAAGCAATCCCTGCTGAGTTCCTTACGTTAGATGCCCTGAGCCCTCAT 128

Db 108 CAGGCAAGCAATCCCTGCTGAGTTCCTTACGTTAGATGCCCTGAGCCCTCAT 167

QY 129 CTCGAGGAGATCATGACCTTCACACACCAAGCACCATCAGACTTATGTTAAGCCCT 188

Db 168 CACGCGGAGATCATGACCTTCACACACCAAGCACCATCAGACTTATGTTAAGCCCT 227

QY 189 CAACGCTGCGGAGGAGAGTCTCGGCGCTGTGGCAAGGAGGATGTGTTACCCAGGT 248

Db 228 GACGTCACGAGGAGAGTACGAGGAGGCTTCCGCAAGGAGATGTACAGCCAGAT 287

QY 249 TAAGCTTCAGTCTGCTCAAGTTCAACGAGGAGGAGACATCAATCACTCTCTGTTCTG 308

Db 288 AGCTCTTCAGCCTGCACCTGAAGTTCAATGGTGGTGCATATCAATCATAGCATTTCTG 347

QY 309 GAAGAACTTGGCTCCCTATGATCCGAGGAGGCTACCTCTCTCAAGGACCTCTCAAGAA 368

Db 348 GACAAACCTCAGCCCTAAACGGTGGTGAGAACCA-----AAGGGAGTTGCTGGA 398

QY 369 GGCTATCGAGGAATCTTTGGTCTTTTCGAGGCTTCAAGAAAGTTCAACGCTGACAC 428

Db 399 AGCCATCAACGCTGACTTTGGTCCCTTGACAAAGTTTAAAGGAAGCTGACGGCTGCATC 458

QY 429 CGTGTGCTCCAGGATCCGAGTGGGCTGGCTTGAACCCGCTTACTAAGAGCT 488

Db 459 TGTGTGTGTCGAAGGCTCAGTTGGGTTGGCTTGTGTTCAATAAGCAACGGGACACTT 518

QY 489 GGAAGTCACACACCGCCCAACGAGGACCTCTGC-----TTACTCACATTCCTAT 539

Db 519 ACAATTCGCTGTGTCCAAATCAGGATCCACTGCAAGGAACACAGGCCCTTATCCACT 578

QY 540 CATCGAGTTGACATCTGGGAGCAGCTTTCTACCTTCAGTACAAGAACGCTCAAGCCCTGA 599

Db 579 GCTGGGATTTGATGTGTGGGAGCAGCTTACTACCTTCAGTATAAAATGTCAAGCCCTGA 638

QY 600 CTATCTCGCTGCTTGTGGTCCGTTTCACTCAACGAGGAGGAGCCCGATTGCGAGG 659

Db 639 TTATCTAAAGCTATTGGAATGTAATCAACTGGGAGATGTAACTGAAAGATACATGGC 698

QY 660 T 660

Db 699 T 699

RESULT 15

ABN84891

ID ABN84891 standard; cDNA; 849 BP.

XX

XX

XX

GenCore version 5.1.6
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Searched: 3470272 seqs, 21671516995 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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6	258.8	38.7	704	8	GMU56403	Ganoderma
7	252	37.7	728	6	E15568	cDNA encodi
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11	246.6	36.9	621	8	AF114848	Paxillus
12	220.6	33.0	630	6	AR222775	Sequence
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ALIGNMENTS

RESULT 1	AX128479	AX128479	669 bp	DNA	linear	FAT 15-MAY-2001
LOCUS	Sequence 4 from Patent EP1111067.					
DEFINITION	AX128479					
ACCESSION	AX128479.1	GI:14134946				
VERSION						
KEYWORDS	Xanthophyllomyces dendrorhous (anamorph: Phaffia rhodozyma)					
SOURCE	Xanthophyllomyces dendrorhous					
ORGANISM	Eukaryota; Fungi; Basidiomycota; Hymenomycetes;					
	Xanthophyllomycetes; Tremellomycetidae; Cystofilobasidiales;					
	Cystofilobasidiaceae; Xanthophyllomycetes.					
REFERENCE	1					
AUTHORS	Hoshino, T., Ojima, K. and Setoguchi, Y.					
TITLE	Recombinant production of carotenoids, particularly astaxanthin					

JOURNAL Patent: EP 1111067-A 4 27-JUN-2001;

F. HOFFMANN-LA ROCHE AG (CH)

FEATURES

source

Location/Qualifiers

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/mol_type="unassigned DNA"

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/notes="unnamed protein product"

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QAL"

ORIGIN

Query Match 100.0%; Score 669; DB 6; Length 669;
Best Local Similarity 100.0%; Pred. No. 5,3e-168;
Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 CCTCCATCTCCAAGGAGATCATGCCCTTCCACCAACCAAGCACCATCAGACTTATGTT 180

DB 121 CCTCCATCTCCAAGGAGATCATGCCCTTCCACCAACCAAGCACCATCAGACTTATGTT 180

QY 181 AACGCTCTCAAGCTCGCGAGGAGAGTACTCGGCGCTGTGGCAAGGAGGATGCTT 240

DB 181 AACGCTCTCAAGCTCGCGAGGAGAGTACTCGGCGCTGTGGCAAGGAGGATGCTT 240

QY 241 ACCGAGGTTAAGCTTCAGTCTGCTCTCAAGTTCAACGAGGAGGACACATCAATCACT 300

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DB 301 CTGTTCTCGAAGAACTTGGCTCCCTATGGATCCGAGGAGGCTTACCTCTCTCAAGGACT 360

QY 361 CTCAGAGGCTATCGAGGAATCTTTGGTTCTTTTCGAGGCTTCAAGAGAGTTCAAC 420

DB 361 CTCAGAGGCTATCGAGGAATCTTTGGTTCTTTTCGAGGCTTCAAGAGAGTTCAAC 420

QY 421 GCTGACACCGCTGCTGTCGAGGATCCCGATGGGCTGCTTGGCTTGAACCCGCTTACT 480

DB 421 GCTGACACCGCTGCTGTCGAGGATCCCGATGGGCTGCTTGGCTTGAACCCGCTTACT 480

QY 481 AAGAGCTGGAAGTACCAACGACCGCAACGAGGACCTCTGCTTACTTCAATCTCTATC 540

DB 481 AAGAGCTGGAAGTACCAACGACCGCAACGAGGACCTCTGCTTACTTCAATCTCTATC 540

QY 541 ATCGAGGTTGACATCTGGAGCAGCTTTTACCTTCACTTCACTTCACTTCACTTCACT 600

DB 541 ATCGAGGTTGACATCTGGAGCAGCTTTTACCTTCACTTCACTTCACTTCACTTCACT 600

QY 601 TATCTCGCTGCTGTTTGGTTCGCTTATCAACTTACAGGAGGAGGCGGCGGCTTCAAGCT 660

DB 601 TATCTCGCTGCTGTTTGGTTCGCTTATCAACTTACAGGAGGAGGCGGCGGCTTCAAGCT 660

QY 661 GCTCTCTAA 669

DB 661 GCTCTCTAA 669

RESULT 2

BD015713

LOCUS

DEFINITION

Recombination production of carotenoids, in particular, astaxanthin.

BD015713

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BD015713 669 bp DNA linear PAT 27-AUG-2002
Recombination production of carotenoids, in particular, astaxanthin.

BD015713

BD015713.1 GI:22556850

JP 2001190294-A/4

Xanthophyllomyces dendrorhous (anamorph: Phaffia rhodozyma)

Xanthophyllomyces dendrorhous

Eukaryota; Fungi; Basidiomycota; Hymenomycetes;

Heterobasidiomycetes; Tremellomycetidae; Cystofilobasidiales;

Cystofilobasidiaceae; Xanthophyllomyces.

1 (bases 1 to 669)

Hoshino, T.; Ojima, K. and Setoguchi, Y.

Recombination production of carotenoids, in particular, astaxanthin

Patent: JP 2001190294-A 4 17-JUL-2001;

F HOFFMANN LA ROCHE AG

OS Phaffia rhodozyma

PN JP 2001190294-A/4

PD 17-JUL-2001

PF 01-DEC-2000 JP 2000367099

PR 01-DEC-1999 EP 99123821.3

PI TATSUO HOSHINO, KAZUYUKI OJIMA, YUTAKA SETOGUCHI PC

CI2N15/09, CI2N1/15, CI2N1/19, CI2N1/21, CI2P23/00, CI2O1/68// PC

(CI2P23/00, CI2R1:01), (CI2P23/00, CI2R1:18), (CI2P23/00, CI2R1:20), PC

(CI2P23/00, CI2R1:465), (CI2P23/00, CI2R1:645), CI2N15/00 CC

Recombination production of carotenoids, in particular, CC

astaxanthin

PH Key Location/Qualifiers

FT CDS (1)..(669).

FEATURES

source

Location/Qualifiers

1..669

/organism="Xanthophyllomyces dendrorhous"

/mol_type="genomic DNA"

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ORIGIN

Query Match

Best Local Similarity 100.0%; Score 669; DB 6; Length 669;

Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGTCGTGTCGAGCATCCCTCTCTCCGTCGTCTAGACAGACTTCGTCGCTCTGCTGCT 60

QY 61 TTCCAGATCAGGCAAGCATACCTGCTGAGCTTCCTTACGCTTACGATCCCTGGAG 120

DB 61 TTCCAGATCAGGCAAGCATACCTGCTGAGCTTCCTTACGCTTACGATCCCTGGAG 120

QY 121 CCTCCATCTCCAAGGAGATCATGCCCTTCCACCAACCAAGCACCATCAGACTTATGTT 180

DB 121 CCTCCATCTCCAAGGAGATCATGCCCTTCCACCAACCAAGCACCATCAGACTTATGTT 180

QY 181 AACGCTCTCAAGCTCGCGAGGAGTACTCGGCGCTGTGGCAAGGAGGATGCTT 240

DB 181 AACGCTCTCAAGCTCGCGAGGAGTACTCGGCGCTGTGGCAAGGAGGATGCTT 240

QY 241 ACCGAGGTTAAGCTTCAGTCTGCTCTCAAGTTCAACGAGGAGGACACATCAATCACT 300

DB 241 ACCGAGGTTAAGCTTCAGTCTGCTCTCAAGTTCAACGAGGAGGACACATCAATCACT 300

QY 301 CTGTTCTCGAAGAACTTGGCTCCCTATGGATCCGAGGAGGCTTACCTCTCTGAAGGACT 360

DB 301 CTGTTCTCGAAGAACTTGGCTCCCTATGGATCCGAGGAGGCTTACCTCTCTGAAGGACT 360

QY 361 CTCAAGAGGCTATCGAGGAATCTTTGGTTCTTTTCGAGGCTTCAAGAGAGTTCAAC 420

DB 361 CTCAAGAGGCTATCGAGGAATCTTTGGTTCTTTTCGAGGCTTCAAGAGAGTTCAAC 420

QY 421 GCTGACACCGCTGCTGTCGAGGATCCCGATGGGCTGCTTGGCTTGAACCCGCTTACT 480

DB 421 GCTGACACCGCTGCTGTCGAGGATCCCGATGGGCTGCTTGGCTTGAACCCGCTTACT 480

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Db	292	GCCAT	CGACAAGACATTGGATCCTTCGAGGAGTTCAAAGAAGAGTTCAACACTGTGTTACT	351
QY	430	GCTGCT	GTCCAAGATCCGGATGGGCTGGCTTGGCTTGAACCCGCTTACTAAGAAGCTG	489
Db	352	CTCGGT	GTCCAGGATCTGGATCGGATGGCTCGGATACAACCGCTACAAGCACCTC	411
QY	490	GAAGT	CACACAGACCGCAACAGGACCCCTGCTTACTCACATTCCTATCATCGAGTT	549
Db	412	GAGAT	CGCCACACCGCCAAACAGGATCCCTTATCACTTTGACTCCCATCATTTGGTCTT	471
QY	550	GACAT	CTGGGAGCACGCTTTTCTACCTTCAGTACAAGAACGCTCAAGCTGACTATCTCGCT	609
Db	472	GACAT	CTGGGAGCACGCTTTTCTACCTCCAGTACAAGAAATGTCGAAGCTGATTACCTTGGC	531
QY	610	GCTGTT	TGGTCCGTTATCAACTCAAGGAGCGAGCCCGATTCGAGGCTGCTCTCTA	668
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DEFINITION			Recombination production of carotenoids, in particular, astaxanthin.	
ACCESSION	BD015714			
VERSION	BD015714.1	GI:22556851		
KEYWORDS	JP 2001190294-A/5.			
SOURCE	Xanthophyllomyces dendrorhous (anamorph: Phaffia rhodozyma)			
ORGANISM	Xanthophyllomyces dendrorhous			
REFERENCE	Eukaryota; Fungi; Basidiomycota; Hymenomycetes;			
AUTHORS	Heterobasidiomycetes; Tremellomycetidae; Cystofilobasidiales;			
TITLE	Cystofilobasidiaceae; Xanthophyllomyces.			
JOURNAL	1 (bases 1 to 597)			
COMMENT	Hoshino,T., Ojima,K. and Setoguchi,Y. Recombination production of carotenoids, in particular, astaxanthin Patent: JP 2001190294-A 5 17-JUL-2001; F HOFFMANN LA ROCHE AG OS Phaffia rhodozyma PN JP 2001190294-A/5 PD 17-JUL-2001 PF 01-DEC-2000 JP 2000367099 PI TATSUO HOSHINO,KAZUYUKI OJIMA,YUTAKA SETOGUCHI PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12P23/00,C12Q1/68// PC (C12P23/00,C12R1:01),(C12P23/00,C12R1:18),(C12P23/00,C12R1:20), PC (C12P23/00,C12R1:465),(C12P23/00,C12R1:645),C12N15/00 CC Recombination production of carotenoids, in particular, CC astaxanthin FH Key Location/Qualifiers FT CDS Location/Qualifiers 1..597 /organism="Xanthophyllomyces dendrorhous" /mol_type="genomic DNA" /db_xref="taxon:5421"			
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SOURCE				
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Best Local Similarity		72.0%;	Pred. No. 1e-73;	
Matches 431;	Conservative	0;	Mismatches 159;	Indels 9; Gaps 1
QY	70	AGGGCA	AAGCATPACCCCTGCCTGAGCTTCCTTACGCTTAGATGCCCTGGAGCCCTCCATC	129
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QY	130	TCAAGG	ATCATGATGACCCCTTACCACACAGCACCATCAGACTTATGTTAAACGGCTC	189
Db	61	TCTAAG	GAATCATGATCTCTTACCACCTCAAGACCATCAGACTTACGTCACCACTC	120

QY 190 AAGCTGCGGAGGAGAGCTACTCGGCGCTGTGGCAAGGAGGATGCTTACCCAGGTT 249
 Db |||||
 121 AAGCGCGCTATCCAGGCTTCTCCAGACCAATGACATCAAG-----CCAGATC 171
 QY 250 AAGCTTCAGTCTCTCTCAAGTTCAACGGAGGAGGACATCAATCACTCTCTGTTCTGG 309
 Db |||||
 172 GCTCTTCAGAGCGCTCTCAAGTTCAACGGAGGAGGACATCAACCACTCCCTCTTCTGG 231
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 Db |||||
 232 AAGAACTGGCTCTCGCGACTCTGTGATGCCAAGCTACCGAGGATCGCTCAAGACT 291
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 Db |||||
 292 GCATCGACAAGGACTTTGGATCTTTCGAGGAGTTCAAGAAGAAAGTTCAACACTGCTACT 351
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 Db |||||
 352 CTCGGTGTCCAGGATCTGTGATGGGATGGCTCGGATACAACACCGCTACCAAGCACCTC 411
 QY 490 GAAGTCAACACGACCGCCCAACAGGACCTCTGCTTACTCAATTCCTATCATCGGAGTT 549
 Db |||||
 412 GAGATCGCCACCAACCGGATCCCTTATCACTTGACTCCCAATCATGCTCT 471
 QY 550 GACATCTGGAGACGCTTTTACCTTCAGTACAAGAACGTTCAAGCCTGACTATCTCGCT 609
 Db |||||
 472 GACATCTGGAGACGCTTTTACCTTCAGTACAAGAACGTTCAAGCCTGACTTACCTTGC 531
 QY 610 GCTGTTTGTCTGTTATCAACTACAAGGAGGAGGAGGCGGCTGATGAGGCTGCTCTCTA 668
 Db |||||
 532 GCTTCTGGAACGCTGCAACTTTGCTGAGGCTCAGCGAAGGTTTGAATGCTGCTGCAA 590

RESULT 5
 AY423629
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AY423629 678 bp mRNA linear PLN 21-OCT-2003
 Cryptococcus bacillisporus MnSOD mRNA, complete cds.
 AY423629.1 GI:37694051
 Cryptococcus bacillisporus (Filobasidiella bacillispora)
 Cryptococcus bacillisporus
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 2 (bases 1 to 678)
 Narasipura, S.D., Chaturvedi, V. and Chaturvedi, S.
 Complete cDNA of MnSOD of Cryptococcus neoformans var. gattii
 Unpublished
 Narasipura, S.D., Chaturvedi, V. and Chaturvedi, S.
 Direct Submission
 Submitted (28-SEP-2003) Mycology, Wadsworth Center, 120 New
 Scotland Ave. Albany, NY 12208, USA

FEATURES
 source

1..678
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CDS

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ORIGIN

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 73 ATTAGGCGCAAGCACACCTTCCCTCTCCCTTATGCTTACGCTTACGATGCCCTGGAGCCCTCC 132
 QY 127 ATCTCAAGGAGATCATGACCTTCCACCAACCAAGCATCAGACTTAATGTAAGGCG 186
 Db |||||
 133 ATCTCTTCTTGAGATTATGAACCTTCCATCAACCAAGCATCACCAGACTTACGTTAAGCGT 192
 QY 187 CTCACACGCTGCCGAGGAGACTACTCGCGGCTGTGGCAAGGAGATGCTTATCCAG 246
 Db |||||
 193 CTTAAGCGCTGTGAGAGTCTCTCAGAAAGCCCTCTGCAGCTGGTGAAGGCTGT 252
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 Db |||||
 253 ATTGCCCTTCAGCCCGCTTCAAAATTCACGGTGGTGGTCAATTAATCACTCTCTCTTC 312
 QY 307 TGGAGAAGCTTGGCTCCCTATGATCCGAGGAGGCTA---CCCTCTCTGAAGACCTCTC 363
 Db |||||
 313 TGGAGAAGCTTGGCTCCCTATGATCCGAGGAGGCTTCCGACCTCCGCTGCTCTTC 372
 QY 364 AAGAAGGCTATCGAGGAATCTTTTGGTTCTTTTCGAGGCTTCAAGAGGAGTCAAGCT 423
 Db |||||
 373 CATGACCCAGCTCAGGCTGACTTTGGTGGCTTCGAAACCTCAAGAAGGAGATGAATGCC 432
 QY 424 GACACGCTGTGTCTCAAGGATCCGAGTGGGCTGGCTTGGCTTGAACCCGCTTACTAAG 483
 Db |||||
 433 AAGACTGTGCTCCATCCAAGGCTCTGTTGGGCTGGCTGGTTACAACAGGACCAAG 492
 QY 484 AAGCTTGGAGTCAACAGACCCCAACAGGACCTCTGCTTACTCAATTCATATCATC 543
 Db |||||
 493 AAGCTCGAGATGTCAACCACTCCCAATCAGGACCTCTCTGTCACGCTCCCTATCAT 552
 QY 544 GAGATTGACATCTGGAGCAGCCTTCTTACCTTCACTACAGCAAGACGTCAGGCTGACTAT 603
 Db |||||
 553 GGCATTGACATCTGGAGCATGCTTTTACCTTCACTTCAAGTCAAGACGTCAGGCTGACTAT 612
 QY 604 CTCGCTGTGTTTGGTCCGTTATCAACTACAAGGAGGAGGCGCCGATTCGAGGCTGCT 663
 Db |||||
 613 CTCACGCGCATCTGGAGCGTTATCACTACGAGGAGGCGGAGAACCGTCTGAAGCTGCC 672
 QY 664 CTCATA 669
 Db |||||
 673 CTGTGA 678

RESULT 6
 GMU56403

LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

GMU56403 704 bp mRNA linear PLN 04-SEP-1996
 Ganoderma microsporum manganese-superoxide dismutase mRNA, complete
 cds.
 U56403
 U56403.1 GI:1519035
 Ganoderma microsporum
 Ganoderma microsporum
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 Apheliales; Ganodermataceae; Ganoderma.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

Wang, H.-F. and Hsueh, R.-S.
 Direct Submission
 Submitted (24-APR-1996) Huei-Fang Wang, Applied Microbiology
 Laboratory/Agricultural Chemistry Department, National Taiwan
 University, Taipei, Taiwan, Republic of China

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

2 (bases 1 to 704)
 Wang, H.-F.
 Studies of Manganese-Superoxide Dismutase Gene of Ganoderma
 Thesis (1996) National Taiwan University, Taipei, Taiwan, Republic
 of China

FEATURES

Location/Qualifiers


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source
1. 704
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ORIGIN
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Best Local Similarity 68.0%; Pred. No. 3.1e-58;
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QY 199 GAGGAGAGTACTCGGCGCTGTGGCAAGGAGATGTTTACCCAGGTTAAGCTTCAG 258
DB 160 GAGGAGGCTTACGCAAGGCTTCACCCCAAGGAGCGCATCGCC-----CTCCAG 210

QY 259 TCTGCTCTCAAGTTCAACGGAGGAGGACACATCAATCACTCTCTGTTCTGGAAGACTTG 318
DB 211 TCGGCCCTCAAGTTCAACGGCGGTGGTACATCAACCACTCCCTCTTCTGGAAGACTT 270

QY 319 GTCCTCTATGATCCGAG-----GAGCTACCTCTCTGAAGACCTTCAAG 366
DB 271 GCCCGCGCAAGTCCGAGGCAAGGCAACGCGCGCGCTCCGCGAGCGGCCCTCAAG 330

QY 367 AAGCTATCGAGGAATCTTTTGGTTCTTCGAGCGCTTCAAGAAGAGTTCAACGCTGAC 426
DB 331 TCTCGGATCGAGAGAACTGGGGCTTCGTGCAACACTTCAAGAGGTTCAAGCGCAC 390

QY 427 ACCGCTGTGTCGAAGGATCGGATGGGGCTGGCTTGGCTTGAACCGCTTACTAAGAG 486
DB 391 ACTGCTGCATCCAGGGCTCTGGCTGGGGCTGGCTCGGACTTAAACCGCAACGAGCGT 450

QY 487 CTGGAAGTCAACAGCGGCAACGAGACCTCTGTTACTCATCATCTTCTATCATCGGA 546
DB 451 CTCGAGATAACGACGCGCAATCAGGACCGCTCTCTCGCATGTCCCATCATCGGC 510

QY 547 GTTGACATCTGGGACGCTTTCTACCTTCAGTACAAGAACGCTCAACGCTGACTATCTC 606
DB 511 GTCGATATCTGGAGCACGCGTTTACTCTCAGTACTCTCAAGTCAAGCGCGACTACCTG 570

QY 607 GCTGCTGTTGGTCCGTTTCACTTCAAGGAGGCGAGGCGCGGATG 654
DB 571 GCGGCGATCGATCGTATCACTTCAAGGAGGCGGAGCGTCTGCTG 618

RESULT 7
LOCUS E15568 728 bp DNA linear PAT 28-JUL-1999
DEFINITION cDNA encoding Malassezia antigen protein MF-3.
ACCESSION E15568
VERSION E15568.1 GI:5710251
KEYWORDS JP 1998077296-A/3.
SOURCE unidentified
ORGANISM unidentified.

```

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REFERENCE
AUTHORS Takesako,K., Daimon,H., Kuroda,M., Katou,I., Yasueda,H., Akiyama,K.
and Yamaguchi,H.
TITLE RECOMBINANT MALASSEZIA ANTIGENIC PROTEIN AND ITS GENE
JOURNAL Patent: JP 1998077296-A 3 24-MAR-1998;
COMMENT TAKARA SHUZO CO LTD
OS Malassezia furfur
PN JP 1998077296-A/3
PD 24-MAR-1998
PP 05-SEP-1996 JP 1996257613
PI TAKESAKO KAZUTADA, DAIMON HISASHI, KURODA MASANOBU, PI KATOU
IKUNOSHIN,
PI YASUEDA HIROSHI, AKIYAMA KAZUO, YAMAGUCHI HIDEYO PC
C07K14/195,A61K39/35,C07H21/04,C07K7/08,C12N15/09,C12Q1/68, PC
G01N33/53,
PC G01N33/569;
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CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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QY 128 TCTCCAAAGGATCATGACCCCTTCCACACACCAAGACCATCAGACTATGTTAAGGCC 187
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QY 188 TCAACGCTGCGAGAGAGTACTCGGCCGCTGTGGCAAGGAGGATGCTTACCAGG 247
DB 128 TCAACGCGCGGAGAGGCTGACGCTGAGGCGAGCGCGGAGGAGGAGGCTTAAAGCAG 187

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QY 308 GGAAGAACTTGGCTCCCTATGATCCGAGAGGCTTACCTCTCTGAAGGACTCTCAAG 367
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QY 368 AGGCTATCGAGGAATCTTTTGGTTCTTTCGAGGCTTCAAGAGAGGTTCAAGCTGACA 427
DB 308 AGGCTATCGAGGAATCTTTTGGTTCTTTCGAGGCTTCAAGAGAGGTTCAAGCTGACA 367

QY 428 CCGCTGCTTCCAAAGGATCCGATGGGCTGCTTGGCTTGAACCCGCTTACTAAGAGC 487
DB 368 CCGCTGCTTCCAAAGGATCCGATGGGCTGCTTGGCTTGAACCCGCTTACTAAGAGC 424

QY 488 TGAAGTCAACACGACCCCAACAGGACCTCTGCTTACTCATTCTATCATTCATCGGAG 547
DB 425 TCGACTGCTGTTGCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 484

QY 548 TTGACATCTGGGAGCAGCTTCTTACCTTCTAGTCAAGAACTGTAAGCTTACTATCTCG 607
DB 548 TTGACATCTGGGAGCAGCTTCTTACCTTCTAGTCAAGAACTGTAAGCTTACTATCTCG 607

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 13:12:34 ; Search time 1718 Seconds

(without alignments)
11628.541 Million cell updates/sec

Title: US-09-727-855B-4

Perfect score: 669

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_man:*

23: em_gss_mus:*

24: em_gss_pro:*

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27: em_gss_vrt:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	284.4	42.5	656	14	CF644174
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4	284.4	42.5	702	14	CF643817

5	267	39.9	617	14	CF643863
6	260.4	38.9	776	14	CA765001
7	221.6	33.1	634	14	CD489102
8	215.6	32.2	606	14	CD271903
9	215.4	32.2	736	14	CF472965
10	212.4	31.7	619	14	CF643518
11	212.2	31.7	730	12	BI904486
12	211	31.5	995	14	CF583893
13	210.8	31.5	746	13	BU060841
14	210.4	31.4	577	14	CD488011
15	209.6	31.3	468	9	AT002967
16	209.6	31.3	539	14	CD272097
17	208.2	31.1	719	12	BG970432
18	208.2	31.1	748	14	CA321590
19	208.2	31.1	825	12	BI412406
20	208.2	31.1	828	14	CD467777
21	208.2	31.1	835	12	BI409485
22	208.2	31.1	867	14	CB590330
23	208.2	31.1	900	11	AK002428
24	208.2	31.1	909	12	BI415463
25	208.2	31.1	914	11	AK012354
26	208.2	31.1	915	13	BY702957
27	208.2	31.1	1001	13	BY703048
28	208.2	31.1	1140	13	BU525570
29	208.2	31.1	1171	11	AK002534
30	207.8	31.1	640	9	AU170704
31	207.8	31.1	643	9	AU169164
32	207.6	31.0	692	14	CB966783
33	207.6	31.0	721	13	BU673715
34	207.2	31.0	538	14	CD270886
35	207.2	31.0	890	13	BU505768
36	206.6	30.9	739	14	CD298026
37	206.6	30.9	830	14	CB668854
38	206	30.8	793	14	CB627323
39	206	30.8	807	14	CB627324
40	206	30.8	826	14	CB668853
41	206	30.8	841	14	CB668027
42	205.8	30.8	556	9	AW064502
43	204.6	30.6	755	14	CB668028
44	204.6	30.6	784	12	BI691345
45	203.8	30.5	901	14	CD459143

ALIGNMENTS

RESULT 1
CF638868
LOCUS
DEFINITION
CF638868
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CF638868 754 bp mRNA linear EST 02-OCT-2003
D08_A03 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA
sequence.
CF638868
EST.
Ustilago maydis
Ustilago maydis
Ustilaginomycetidae; Basidiomycota; Ustilaginomycetes;
Nugent, K.G., Choffe, K. and Saville, B.J.
Gene Expression during Ustilago maydis Diploid Filamentous Growth:
EST Library Creation and Analyses
Unpublished (2003)
Contact: Barry J. Saville
Saville Lab
University of Toronto
3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
Tel: 905 569 4702
Fax: 905 828 3792
Email: bsaville@utoronto.ca
Plate: UTM-UM-D126/7-008-UTM row: 03 column: A
Seq primer: T7 Reverse (5' GAGTAATACGACTCACTATAGG 3')
High quality sequence stop: 754.

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FEATURES
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      1. .754
        /organism="Ustilago maydis"
        /mol_type="mRNA"
        /strain="FBD12"
        /db_xref="taxon:5270"
        /cell_type="Mycelia"
        /dev_stage="Filamentous diploid"
        /clone_lib="Filamentous Forced Diploid"
        /note="Vector: pSport; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."

ORIGIN
  Query Match      42.7%; Score 285.8; DB 14; Length 754;
  Best Local Similarity 66.5%; Pred. No. 1.4e-66;
  Matches 410; Conservative 0; Mismatches 207; Indels 0; Gaps 0;

QY 48 CGCTCTGCTGCTTTCCAGATCAGGGCAAGCATACCTCGCTGAGCTTCCTTACGGCTTA 107
Db 12 CGCGTCCGAATCTCTGCCAAATGCTGAGCACACCTTCCCAGCTCCCTTACGGCTA 71
QY 108 CGATGCCCTGGAGCCCTCCATCTCAAGAGATCATGACCTTCCACCAAGACCA 167
Db 72 CAATGAGCTCGAGCGCGCATCTCGAGGAGATCATGACCATCCACCAAGACCA 131
QY 168 TCAGACTTATGTTAAGCGCTCAACGCTCCGAGGAGACTACTCGGCGCTGTGGCAA 227
Db 132 CCAGTTTACGTCACCAATCTCAACACGCTATCAAGGCTCAACTCGGCCATCTCGAG 191
QY 228 GGAGATGTGCTTACCCAGGTTAAGCTTCAGTCTGCTCTCAAGTTCAACGGAGGAGCA 287
Db 192 CAACAGCTTCGCAAGCAGATTGAGCTCCAGAGCGCATCAAGTTCAACGGCGGTGCCA 251
QY 298 CATCAATCACCTCTGTTCTGGAAGAACTTGCTCCCTATGATCGGAGGAGCTACCT 347
Db 252 CATTAACCACTCGCTCTTCTGGAAGAACTTGCTCTCGCAGCCAGGCGGTGACAGCT 311
QY 348 CTCTGAAGGACCTCTCAAGAGGCTATCGAGGAATCTTTTGGTTCTTTGAGGCGCTCAA 407
Db 312 TCAAGATGTCCTTCAAGCAGCGCGTGAAGCTGACTTTGGCTCGCTCGACAACTCAA 371
QY 408 GAAGAAGTTCAACGCTGACACCGCTGCTGTCAAGGATCGGATGGGCTGGCTTGGCTT 467
Db 372 ATCCACCTTCAACGCTACCAATTGCCACCATCCAGGGCTCTGTTGGGCTGGCTCGGTT 431
QY 468 GAACCGCTTACTAAGAGCTGGAAGTCACACGACCGCCACACGAGGACCTCTGCTTAC 527
Db 432 CAACCCCAAGAACTCGAAGCTTGAGGTTGTCAACCAAGGACCGAGGACCTCTGATCTC 491
QY 528 TCACATTCCTATCATCGGAGTTGACATCTGGAGCACGCTTCTTACCTTCAGTCAAGAA 587
Db 492 GCACACCCCATCATCGTGTGCGAGCTTGGAGCACGCTTCTTACCTCCAGTACAAGAA 551
QY 588 CGTAAAGCTGACTACTCTCAAGAACATTTGGTTCGTTATCAACTCAAGGAGGAGGAGGC 647
Db 552 TGTAAAGCTGACTACTCTCAAGAACATTTGGTTCGTTATCAACTCAAGGAGGAGGAGGGA 611
QY 648 CCGATTGAGGCTGCTC 664
Db 612 CGCTTCAAGGCTGCC 628

RESULT 2
CF644174
LOCUS
DEFINITION
  CF644174
  CF644174
  CF644174.1
  GI:37413160
  EST
  KEYWORDS
  SOURCE
    Ustilago maydis

ORGANISM
  Ustilago maydis
  Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
  Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
  1 (bases 1 to 656)
  Nugent, K.G., Choife, K. and Saville, B.J.
  Gene Expression during Ustilago maydis Diploid Filamentous Growth:
  EST Library Creation and Analyses
  Unpublished (2003)
  Contact: Barry J. Saville
  Saville Lab
  University of Toronto
  3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
  Tel: 905 569 4702
  Fax: 905 828 3792
  Email: bsaville@utoronto.ca
  Plate: UTM-UM-D128/9-017-UTM row: 06 column: G
  Seq primer: T7 Reverse (5' GAGTAATACCACTACTATAGGG 3')
  High quality sequence stop: 656.

FEATURES
  source
    Location/Qualifiers
      1. .656
        /organism="Ustilago maydis"
        /mol_type="mRNA"
        /strain="FBD12"
        /db_xref="taxon:5270"
        /cell_type="Mycelia"
        /dev_stage="Filamentous diploid"
        /clone_lib="Filamentous Forced Diploid"
        /note="Vector: pSport; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."

ORIGIN
  Query Match      42.5%; Score 284.4; DB 14; Length 656;
  Best Local Similarity 66.8%; Pred. No. 3.1e-66;
  Matches 405; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

QY 59 CTTTCCAGATCAGGGCAAGCATACCTCGCTGAGCTTCTTACGCTTACGATGCCCTGG 118
Db 45 CTCCTCCCAAAATGCTTGAGCACACCTTCCCAGCTCCCTTACGCTACATGAGCTCG 104
QY 119 AGCCCTCCATCTCCAAGGAGATCATGACCTTCCACCAAGACCATCAGACTTATG 178
Db 105 AGCCCGCATCTCGGAGGAGATCATGACCATCCACCAAGACCATCAGCTTACG 164
QY 179 TTAAGCGCTCAACGCTCCGAGGAGACTACTCGGCGCTGTGGGAGGAGATGTC 238
Db 165 TCACCAATCTCAACAACGCTATCAAGGCTTCACTCGGCCATCTCGAGCAACGAGTTC 224
QY 239 TTACCCAGGTTAAGCTTCAGTCTGCTCTCAAGTTCAACGGAGGAGGACACATCAATCACT 298
Db 225 GCAGCAGATTGAGCTCCAGAGCGCATCAAGTTCAACGGCGGTGGCCACATTACCACT 284
QY 299 CTCCTGTTCTGAAGAACTTGGCTCCCTATGATCGAGGAGGCTACCTCTCTGAAGGAC 358
Db 285 CGCTCTTCTGAAGAACTTGGCTCCCTGCTGAGCGGCTGGACAGCTTCAAGATGTC 344
QY 359 CTCTCAAGAGGCTATCGAGGAATCTTTGGTTCTTTGAGGCTTCAAGAGAGATTCA 418
Db 345 CTTCAAGCAGGCGCTCGAACGTAAGTCTGCTCGCTCGAACCTCAAAATCCACCTTCA 404
QY 419 ACAGTGCACACCGCTGCTGCCAAGGATCCGGATGGGCTGGCTTGAACCGGCTTA 478
Db 405 ACAGTGCATTCGCCCATCCAGGCTCTGTTGGGCTGGCTCGTTTCAACCCCAAGA 464
QY 479 CTAAAGAGCTGGAAGTCAACACGACCGCCACACCGAGACCTCTGCTTACTCATCTCTA 538
Db 465 ACTCGAGCTTGAAGTGTGTCACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 524
QY 539 TCATCGGAGTTGAGATCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 598
Db 525 TCATCGGAGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 584
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QY 599 ACTATCTGCTGCTGTTTGGTTCGTTATCACTACAAAGGAGGAGAGGCCCGCCGATTCGAGG 658
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 Db 585 ACTACTTCAAGAACATTGTGCTGCTCATCACTTCAAGGAGGCGGAGGCGCTTCAAGG 644
 |||||
 QY 659 CTGCTC 664
 |||||
 Db 645 CTGCCC 650

RESULT 3
 CF643783
 LOCUS
 DEFINITION
 K12_E10 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

CF643783
 662 bp mRNA linear EST 02-OCT-2003
 sequence.
 CF643783
 1 GI:37412406
 EST.
 Ustilago maydis
 Ustilago maydis
 Ustilago maydis
 Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 1 (bases 1 to 662)
 Nugent, K.G., Choffe, K. and Saville, B.J.
 Gene Expression during Ustilago maydis Diploid Filamentous Growth:
 EST Library Creation and Analyses
 Unpublished (2003)
 Contact: Barry J. Saville
 Saville Lab
 University of Toronto
 3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
 Tel: 905 569 4702
 Fax: 905 828 3792
 Email: bsaville@utm.utoronto.ca
 Plate: UTM-UM-D128/9-012-UTM row: 10 column: E
 Seq primer: T7 Reverse (5' GAGTAATACGACTACTATAGGG 3')
 High quality sequence stop: 662.

FEATURES
 source
 1..662
 /organism="Ustilago maydis"
 /mol_type="mRNA"
 /strain="FBD12"
 /db_xref="taxon:5270"
 /cell_type="Mycelia"
 /dev_stage="Filamentous diploid"
 /clone_lib="Filamentous Forced Diploid"
 /note="Vector: pSport; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."

ORIGIN
 Query Match 42.5%; Score 284.4; DB 14; Length 662;
 Best Local Similarity 66.8%; Pred. No. 3.1e-66;
 Matches 405; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

QY 59 CTTCAGATCAGGCGAAGCATACCTCGCTGAGCTTCCTTACGCTTACGATGCCCTGG 118
 |||||
 Db 54 CTCTGCCAAATGTCTGAGCACACCTTCCCGAGCTCCCTTACGCTACATGACTCG 113
 |||||
 QY 119 AGCCCTCCATCTCCAGGAGATCATGACCTTCACCAACCAGACCATCATGACTATG 178
 |||||
 Db 114 AGCCCGCCATCTCGGAGGAGATCATGACCATCCACCAAGACCAACCAAGCTTACG 173
 |||||
 QY 179 TTAAAGCGCTCAACGCTCGCGAGGAGCTACTCGGCCCTGTGGCAAGGAGGATGTC 238
 |||||
 Db 174 TCACCATCTCAACACGCTATCAAGCCCTACACTCGGCCCATCTCGACCAACGAGTTC 233
 |||||
 QY 239 TTACCCAGCTTAAGCTTCAAGTCTGCTCTCAAGTTCAACGGAGGAGGACATCAATCACT 298
 |||||
 Db 234 GCAAGCAGATTGAGTCCAGAGGCCATCAAGTTCAACGGCGGTGGCCACATTACCACT 293
 |||||
 QY 299 CTCTGTTCTGGAAGAACTTGGCTCCCTATGATCGGAGGAGCTACCTCTCTGGAAGGAC 358
 |||||

Db 294 CGCTCTTCTGGAAGAACCTTGTCTCTCCAGCGAGGCGGTGGACAGCTTCAAGATGGTC 353
 |||||
 QY 359 CTCTCAAGAGGCTATCGAGAAATCTTTTGGTTCCTTTTCGAGGCTTCAAGAGAGTTC 418
 |||||
 Db 354 CCTTCAAGCAGGCGCTCGAACGTCGCTTGGCTCGCTCGACAACTCAAAATCCACCTTCA 413
 |||||
 QY 419 ACCTGACACCGCTGCTGTCTCAAGGATCGGATGGGCTTGGCTTGAACCCGCTTA 478
 |||||
 Db 414 ACCTTACCATTGCCACCATCCAGGCTCTGGTGGGCTGGCTGGTTTCAACCCCAAGA 473
 |||||
 QY 479 CTAAAGCTGGAAGTCAACCAAGCCGCAACAGGACCCCTCTGCTTACTCACTTCTTA 538
 |||||
 Db 474 ACTCGAAGCTTGAAGTTGTCAACCAAGGACGAGACCCCTCTGATCTCGCACCCCA 533
 |||||
 QY 539 TCATCGGAGTTGACATCTGGGAGCAGCTTTTACCTTCACTCAAGAGAGCTCAAGCTG 598
 |||||
 Db 534 TCATCGGAGTTGAGCTTGGGAGCAGCTTTTACCTTCAAGAGAGCTCAAGCTTCAAG 593
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 QY 599 ACTATCTCGCTGCTGTTTGGTTCGTTTATCAACTACAGGAGGAGGCGGCCGATTCGAG 658
 |||||
 Db 594 ACTACTTCAAGACATTTGGTCTGTCATCACTTCAAGGAGGCGGAGGCGCTTCAAG 653
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 QY 659 CTGCTC 664
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 Db 654 CTGCCC 659

RESULT 4
 CF643817
 LOCUS
 DEFINITION
 K13_A05 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

CF643817
 702 bp mRNA linear EST 02-OCT-2003
 sequence.
 CF643817
 1 GI:37412471
 EST.
 Ustilago maydis
 Ustilago maydis
 Ustilago maydis
 Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 1 (bases 1 to 702)
 Nugent, K.G., Choffe, K. and Saville, B.J.
 Gene Expression during Ustilago maydis Diploid Filamentous Growth:
 EST Library Creation and Analyses
 Unpublished (2003)
 Contact: Barry J. Saville
 Saville Lab
 University of Toronto
 3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
 Tel: 905 569 4702
 Fax: 905 828 3792
 Email: bsaville@utm.utoronto.ca
 Plate: UTM-UM-D128/9-013-UTM row: 05 column: A
 Seq primer: T7 Reverse (5' GAGTAATACGACTACTATAGGG 3')
 High quality sequence stop: 702.

FEATURES
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 /organism="Ustilago maydis"
 /mol_type="mRNA"
 /strain="FBD12"
 /db_xref="taxon:5270"
 /cell_type="Mycelia"
 /dev_stage="Filamentous diploid"
 /clone_lib="Filamentous Forced Diploid"
 /note="Vector: pSport; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."

ORIGIN
 Query Match 42.5%; Score 284.4; DB 14; Length 702;
 Best Local Similarity 66.8%; Pred. No. 3.3e-66;
 Matches 405; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

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QY 59 CTTTCAGATCAGGCAAGATACCTGCTGAGTTCCTTACGCTTACGATCCCTGG 118
Db 82 CTCTGCCCAAAATGCTTGAGACACACCTTCCAGAGTCCCTTAGCGGTACATGAGCTG 141
QY 119 AGCCTCCATCTCCAGGAGATCATGACCTTCCACCAACCAACCAATCAGACTTATG 178
Db 142 AGCCCGCATCTCGGAGGAGATCATGACCTTCCACCAACCAACCAACCACTTACG 201
QY 179 TTAAGGCGCTCAACGCTCGGAGAGAGACTACTCGGCGCTGTGGGAGAGATGTC 238
Db 202 TCACCAATCTCAACAAGCTATCAAGGCTTAACTCGGCCATCTCGAGCAACGACGTT 261
QY 239 TTACCCAGGTTAAGCTCAGTCTGCTCAAGTTCAACGAGGAGGACACATCAATCACT 298
Db 262 GCAAGCAGATTGAGTCCAGAGCGCCATCAAGTTCAACGCGGTGGCCACATTAACCACT 321
QY 299 CTCTGTCTGGAAGAACTTGGCTCCCTATGATCGGAGGAGCTACCTCTCTGAAGGAC 358
Db 322 CGCTCTCTGGAAGAACTTGGCTCCCTGAGGAGGAGGCTGAGAGCTTCAAGATGTC 381
QY 359 CTCTCAAGAGGCTATCGAGAACTTTTGGTCTTTGAGGCTTCAAGAGAGTTCA 418
Db 382 CTTTCAAGAGGCGCTGAAAGCTGACTTTGGCTGCTCGCAACCTCAAAATCCACCTTCA 441
QY 419 ACCTGTACACCGCTGCTGCTCAAGATCGGATGGGCTGGCTTGGCTTGAACCGCTTA 478
Db 442 ACCTGTACATTTGCCACCATCAGGCTCTGGTTGGGCTGGCTGGTTTCAACCCCAAGA 501
QY 479 CTAAGAAGCTGGAAGTCAACCAAGCGCCCAACGAGGACCTCTGCTTACTCACATTCCTA 538
Db 502 ACTCGAAGCTTGAGTTGCTCAACCAAGGAGGAGGAGGCTGATCTCGACACCCCA 561
QY 539 TCATCGGAGTTGACATCTGGAGAGCGCTTCTTACTCTTCAAGAGAGCTCAAGCGCTG 598
Db 562 TCATCGGTTGCGAGCTTGGAGCAGCTTCTTACTCTCAGTACAGAAATGTTAAGGCTG 621
QY 599 ACTATCTCGCTGCTGTTTGGTCCGTTATCAACTACAGGAGGAGGAGGCGGATTCAGG 658
Db 622 ACTACTTCAAGAACATTTGGTTCGTTCACTCACTTCAAGGAGGCGGAGGAGGCTTCAAG 681
QY 659 CTGCTC 664
Db 682 CTGCCC 687

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RESULT 5
LOCUS CF643863
DEFINITION K13 E08 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA
sequence.
CF643863
VERSION CF643863.1 GI:37412562
KEYWORDS EST.
SOURCE Ustilago maydis
ORGANISM Ustilago maydis
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.

```

```

1 (bases 1 to 617)
Nugent, K.G., Choife, K. and Saville, B.J.
Gene Expression during Ustilago maydis Diploid Filamentous Growth:
EST Library Creation and Analyses
Unpublished (2003)
Contact: Barry J. Saville
Saville Lab

```

```

REFERENCE University of Toronto
AUTHORS 3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
TITLE Tel: 905 569 4702
JOURNAL Fax: 905 828 3792
COMMENT Email: bsaville@utoronto.ca
Plate: UTM-UM-D128/9-013-UTM Row: 08 Column: E
Seq primer: T7 Reverse (5' GAGTAATACGACTACATATAGG 3')
High quality sequence stop: 617.
Location/Qualifiers

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source

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1. 617
/organism="Ustilago maydis"
/mol_type="mRNA"
/strain="PBD12"
/db_xref="taxon:5270"
/cell_type="Mycelia"
/dev_stage="Filamentous Forced Diploid"
/clone_lib="Filamentous Forced Diploid"
/notes="Vector: pSport; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."

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ORIGIN

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Query Match 39.9%; Score 267; DB 14; Length 617;
Best Local Similarity 66.3%; Pred. No. 1.6e-61;
Matches 384; Conservative 0; Mismatches 195; Indels 0; Gaps 0;
QY 28 GTGTCTAGACAGATTGCTGCTGCTGCTTCCAGATCAGGCAAGATACCCCTG 87
Db 35 CGCTCGTCGCGCAGTTTGTGCGCTCTGCCCTCGCGCCGTGCGAGCCAAACACACGCTT 94
QY 88 CTTGAGCTTCTTACGCTTACGATGCTGAGGCTCCATCTCCAGAGATCATGACC 147
Db 95 CCGACCTGGCTTTCGACTACGGTGCACTGAGCGCCGCTTTCATCCAGATCATGAG 154
QY 148 CTTACACACACCAAGCACCATCAGACTTATGTTAAAGCCCTCAACGCTGCCGAGGAGAGC 207
Db 155 CTACACACACCAAGCACCATCAGACTTATGTTAAAGCCCTCAACGCTGCCGAGGAGAGC 214
QY 208 TACTCGGCGCTGTGGGCAAGGAGATGTCTTACCCAGGTTAAGCTTCAAGTCTGCTCTC 267
Db 215 CTCTCTGAAGCGATCCACAGAGAGGACGTCAGTCCGCAATCGCTCTTTCAGAAAGCGATC 274
QY 268 AAGTTCACGAGGAGGAGACATCAATCACTCTCTGTTCTGGAAGAACTTGGCTCCCTAT 327
Db 275 AACTTTAAGCGCGGTGTCATCAACCACTCTCTTTGGGAGAACTTGGCCCGGAG 334
QY 328 GGATCCGAGGAGGCTTACCCCTCTCTGAAGAGACCTCTCAAGAGGCTTATCGAGGAATCTTTT 387
Db 335 AAGATGCGGCTGTGAGTGTGAGCAGCGCGCTCTCAAGGAGCTTATCGACGAGACTTT 394
QY 388 GGTCTTTTCGAGGCTTCAAGAGAGTTCAACGCTGACACGCTGCTGTCTCAAGGATCC 447
Db 395 GGTGTTTGGACCAAGTCCAAAGTTCAATGCTCAGATCGCTGCCATCCAGGTTCC 454
QY 448 GGATCGGCTGCTTGGCTTGAACCGCTTACTTAAGAGCTGGAAGTCAACACGACCGCC 507
Db 455 GGTGCGGTTGGCTCGGCTACAAACCGGAGACCAAGAGCTCGACATGTCTACTACCGCC 514
QY 508 AACCAGGACCTCTCTTACTTACATTCCTATCATCGGAGTTGACATCTGGGAGACGCT 567
Db 515 AACCAGGACCTCTCTCTCGCATGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 574
QY 568 TTCTACCTTCAGTACAGAACGCTAAGCTGACTATCTC 606
Db 575 TTCTACCTTCAGTACAGAACGCTAAGCGCGACTATCTC 613

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RESULT 6
LOCUS CA765001
DEFINITION

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ACCESSION CA765001
VERSION CA765001.2 GI:27546712
SOURCE EST.
ORGANISM Oriza sativa (indica cultivar-group)

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Oriza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

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CA765001 776 bp mRNA linear EST 08-JAN-2003
AF53-Rpf_05_M09_T7_039.ab1 IRRI Drought Stress Panicle Library
Oriza sativa (indica cultivar-group) cDNA clone C0001833 5' similar
to Superoxide dismutase [Mn], mitochondrial precursor (EC
1.15.1.1), mRNA sequence.

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CA765001
CA765001.2 GI:27546712

```

REFERENCE
1 (bases 1 to 776)
Bennett, J., Arumugam, K., Lafitte, R., Wen, J., Rudd, S. and
Bruskiewich, R.M.

TITLE
JOURNAL
COMMENT
IRRI Drought Stress Panicle cDNA Library
Unpublished (2002)
On Dec 2, 2002 this sequence version replaced gi:25994256.

Contact: Richard Bruskiewich
Biometrics and Bioinformatics Unit
International Rice Research Institute
DAPO 7777, Metro Manila, Philippines
Tel: +63-2-845-0563
Fax: +63-2-845-0606

Email: r.bruskiewich@cgiar.org
International Rice Information System (IRIS;
http://www.iris.irri.org): D0201832

Assignment of putative function to the sequence by S. Rudd of the
Munich Information Center for Protein Sequences
(http://mips.gsf.de)

Plate: 05 row: M column: 09.

Location/Qualifiers

1..776
/organism="Oryza sativa (indica cultivar-group)"

/mol_type="mRNA"

/cultivar="IR64"

/db_xref="taxon:39946"

/clone="C0001833"

/tissue_type="Panicles"

/dev_stage="Flowering"

/clone_lib="IRRI Drought Stress Panicle Library"

/note="Vector: plasmid II SK+; Water stress was
applied by not watering for 4 consecutive days. Panicles
were collected from control (well watered) and stressed
plants at 2 days before heading, at heading, 50% flowering
and 4 days after 50% flowering."

ORIGIN

Query Match 38.9%; Score 260.4; DB 14; Length 776;
Best Local Similarity 65.1%; Pred. No. 1.2e-59;
Matches 385; Conservative 0; Mismatches 203; Indels 3; Gaps 1;
QY 71 GGGCAAGCATACCTCGCTGAGTTCCTTACGCTTACGATGCGCTCGAGCCCTCCCATCT 130
Db 162 GCGGACAGCACACCTCGCTGAGTTCCTCGTACGCTATGATGCGCTCGAGCGGCTCATCT 221

QY 131 CCAAGGATCATGACCTTCCACACACCAAGGAGGATGCTTACCCAGGTTA 190

Db 222 NGAAGGAGATCATGACGCTCCACACACCAAGCACCAGACCTACGTCATGGCCCTCA 281

QY 191 ACGCTGCGGAGGAGGCTACTCGGCGCTGTGGCAAGGAGGATGCTTACCCAGGTTA 250

Db 282 ATGCGCGGAGAGAGAGCGCGCCAGTTTCAACAGTCGGGCGAGCTCAAGCGGAGATCA 341

QY 251 AGCTTACGTCGTCTCAAGTTCAACGAGGAGGAGACATCAATPACTCTCTGTCTGGA 310

Db 342 ATTTCAGGCGCGCTTGAAGTTTAAAGGCTGAGGCTGACCTGCTCTCTCTGCG 401

QY 311 AGACTTGGCTCCCTATGGATCCGAGGAGGCTACCTCTCTGAAGGAC---CTCTCAAGA 367

Db 402 GCAACCTCGGCGGACCGGACTCGGCGCTACCAAGCCGGAAGCGCTCCGACCTTTATCA 461

QY 368 AGGCTATCGAGGAATCTTTTGGTCTTTTCGAGGCTTTCAGAGAAGTTCAGCGCTGACA 427

Db 462 AGCAGTCTGAAGGACTTTTGGATCCCTCGAGGCGCTCAAGATGAATCAACACCAAGA 521

QY 428 CCGCTGCTGTCTCAAGATTCGGATGGGCTGGCTTGGCTTGAACCCGCTTACTAAGAAGC 487

Db 522 CGGCGCGATCCAGGATCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 581

QY 488 TGAAGTCAACACGACCGCAACAGGAGCCCTCTGCTTACTTCACTTCCCTATCATCGGAG 547

Db 582 TGGACGTGGTCTACTTACTGCAACAGGAGCCCTNGTNGTGACTCAGGAGGCAATCTCGTA 641

QY 548 TTGACATCTGGAGCAGCGCTTCTACCTTCAGTACAAAGACGTCAGCTGACTATCTCG 607
Db 642 TCGACATCTGNAACACGCGTCTACTTGTGAGTACAGATGTCAAGCTGACTACCTCA 701
QY 608 CTGCTGTTTGGTCCGTTATCAACTACAGGAGGAGGCGGCGGCTTGCAGG 658
Db 702 AGGCCATCTGGAACGTNATCAACTTTGAAANATCGAANAAGCGCTTTNAAG 752

RESULT 7

CD489102

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Ustilago maydis

Ustilago maydis

Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;

Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.

1 (bases 1 to 634)

Sacadura, N.T. and Saville, B.J.

Gene expression and EST analyses of Ustilago maydis germinating

teliospores

Fungal Genet. Biol. 40 (1), 47-64 (2003)

22829673

12948513

COMMENT

Contact: Barry J. Saville

Saville Lab

University of Toronto

3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada

Tel: 905 569 4702

Fax: 905 828 3792

Email: bsaville@utoronto.ca

Seq primer: M13 reverse primer (5' AACAGCTATGACCATGTTC 3').

Location/Qualifiers

1..634

/organism="Ustilago maydis"

/mol_type="mRNA"

/strain="PBI/PB2"

/db_xref="taxon:5270"

/cell_type="Teliospore"

/dev_stage="Germinating teliospore"

/lab_host="E. coli"

/clone_lib="Teliospore"

/notes="Vector: pDNR-LIB; Site 1: SfiIA; Site 2: SfiIB;

mRNA was extracted from germinating teliospores. cDNA was

amplified by PCR and unidirectionally cloned into pDNR-LIB

plasmid, with the use of Clontech's Creator SMART cDNA

Library Construction Kit."

ORIGIN

Query Match 33.1%; Score 221.6; DB 14; Length 634;
Best Local Similarity 65.0%; Pred. No. 3.9e-49;
Matches 357; Conservative 0; Mismatches 190; Indels 2; Gaps 2;
QY 28 GTGCTAGACAGACTTTCGTCGCTCCGCTGCTTTCAGATCAGGCGCAAGCATACCTG 87
Db 78 GCSTGCTGCGCGAGTTTGTGCGCTCTCGGCCCTGCGGAGCAAGCACACGCTT 137
QY 88 CTTGAGCTTCTTACGCTTACGATGCGCTCGAGCCCTCCATCTCCAAGGAGATCATGACC 147
Db 138 CCGACCTGCTTTCGACTACGCTGACTCGAGCCCGCAITTCATCCAAGATCATGGAG 197
QY 148 CTTCAACACCAAGCACCACATCAGCTTATGTTAAACGGCTTCAACGCTCGCGGAGGAGC 207
Db 198 CTACACCAACCAAGCACCACAGCCTATGTCAACGCTCTCAACGAGCGGAGAGCAG 257
QY 208 TACTCGGCCCTGTGGCAAGGAGATGCTCTTACCCAGGTTAAGCTTCTGCTCTCTC 267
Db 258 CTCTCTGAAGCGATCCACAAGAGAGAGCTCAAGTCGGCAATCGCTCTTCAGAAGCGATC 317
QY 268 AAGTTCAACGAGGAGGAGACATCACTCTCTGTCTTGGAGAACTTGGCTCCCTAT 327

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Db 318 AACCTTAACGGCGGTGGTACATCAACACACTCTCTTTTGGGAAATCGCCCGCAG 377
Qy 328 GGATCCGAGGAGCTACCTCTCTGAAGGACTCTCAAGAAGGCTATCGAGGAATCTTTT 387
Db 378 AAGAAATGGCGGTGGTGGAGTTGAGCGCGCGCTCTCAAGGACGCTATCGACGAGACTTT 437
Qy 388 GGTCTTTCTGAGCGCTTCAAGAAGAGTTCAACGCTGACACCGCTGCTGTCTCAAGG-ATC 446
Db 438 GGTGGTTGGACAGCTCAAGTCCAGTTCAATGCTCAGATCGCTGCCATCCAGGGTTTC 497
Qy 447 CGATGGGGCTGGCTTGAACCCGCTTACTAAGAAGCTGGAAGTCAACACACCGC 506
Db 498 CGTTTGGGGTGGCTCGGCTACAAACCGCAGACCAAGAGTCTGACATTGTCACTACCGC 557
Qy 507 CAACAGGAGCCCTCTGCTTACTCACAATTCCTAT-CATCGGAGTTGACATCTGGGACAG 565
Db 558 CAACAGGAGCCCTCTGCTCTCGCATGGGCTCTGNATCGGGTGCAGCGTTGGGAACATG 617
Qy 566 CTTTCTACC 574
Db 618 CTTTCTACC 626

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CD271903 606 bp mRNA linear EST 01-SEP-2003
T143A01367F (FHIG:A) Ectomycorrhiza plate culture Betula
pendula/Paxillus involutus mixed EST library cDNA 5', mRNA
sequence.
CD271903
CD271903.1 GI:34383949
EST.
Betula pendula/Paxillus involutus mixed EST library
Betula pendula/Paxillus involutus mixed EST library
Eukaryota; mixed EST libraries.
1 (bases 1 to 606)
Johansson,T., Le Quere,A., Ahren,D., Soderstrom,B., Erlandsson,R.,
Lundberg,J., Uhlen,M., and Tundl,A.
Transcriptional responses of Paxillus involutus and Betula pendula
during formation of ectomycorrhizal root tissue
Unpublished (2003)
Contact: Johansson,T.
Fungal-Host Interaction Group (FHIG)
Microbial Ecology, Institution of Ecology
Ecology Building, Lund University, SE-223 62 Lund, Sweden
Tel: +46 46 222 45 49
Fax: +46 46 222 41 58
Email: tomas.johansson@mbioekol.lu.se
PCR Primers
FORWARD: P104 (5'-GGGAAGCGCGCCATTGTGT-3')
BACKWARD: P105 (5'-AGTGAGCTGAATGCGGC-3')
Seq primer: P104
High quality sequence stop: 606.
Location/Qualifiers
1. .606
/organism="Betula pendula/Paxillus involutus mixed EST
library"
/mol_type="mRNA"
/strain="ATCC200175 (P. involutus);Skuleskogen,Skogsforsk,Sw
eden(B.pendula)"
/db_xref="taxon:231415"
/tissue_type="Ectomycorrhizal root tissue"
/dev_stage="25 days of growth after transfer/synthesis"
/lab_host="Escherichia coli BM25.8"
/clone_lib="FHIG:A) Ectomycorrhiza plate culture"
/note="Vector: pTriplex2; Site: 1: SfiI; Site 2: SfiI; This
EST clone is originating from one of three cDNA libraries,
constructed for transcript profiling of the mycorrhizal
interaction between the basidiomycete Paxillus involutus
and Betula pendula (birch). One library represents the
developed and functional mycorrhizal root tissue
(FHIG:A) Ectomycorrhiza plate culture", a second

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RESULT 8
CD271903
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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FEATURES
source

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ORIGIN
Query Match 32.2%; Score 215.6; DB 14; Length 606;
Best Local Similarity 65.1%; Pred. No. 1.6e-47;
Matches 376; Conservative 0; Mismatches 179; Indels 23; Gaps 3;
Qy 72 GGCAGAGATACCCCTGCTGAGCTTCTTACGTTACGATCCCTGGAGCCCTCCATCTC 131
Db 31 GGGCCAAACACACTCTCCCGACCTCCCGTACTCTATGATGCTCTGAGCCCTTACATCTC 90
Qy 132 CAAGGAGATCATGACCTTCCACCAACCAAGCACCATCAGACTTATGTTAAAGCCCTCAA 191
Db 91 GCAGCAGATCATGAGCTTCCACCAAGAGCACCACCAACTATGCTACTGCTCTCAA 150
Qy 192 CGCTCCGAGGAGAGCTACTCGGCGCTGTGGCGAGGAGATGCTTACCAGGTTAA 251
Db 151 CGCGCTGAAGTCAGTTACGC-----GAACTGCTACTCCCAAGGAGCGCATCGC 200
Qy 252 GCTTCAGTCTCTCTCAAGTTCAACGAGGAGGAGACATCACTCTCTGTTCTGGAA 311
Db 201 CTTCAAGCTGCGCTCCGCTTCAACGCTGCTGATATCAACCACTCTCTCTCTCGGAA 260
Qy 312 GAATTTGGCTCTCTATGGATCG-----AGGAGGCTACCTCTCTGAAGGACC 359
Db 261 GAACCTTGACCTGCTGTAGCGAGGCAAGGCGAGGAGCTCAACCTGGCCC 320
Qy 360 TCTCAAGAGGCTATCGAGGAATCTTTGGTCTTTTCGAGGCTTCAAGAAGATTCOA 419
Db 321 ATTGAAGATGCTCATCGACTCGAACTTTGGCTCGCTCGATAGCTCAAGAAGATTCOA 380
Qy 420 CGCTGACACCGCTGCTCCAGAGTCCGATGGGCTGCTTGGCTTGAACCCGCTTAC 479
Db 381 TGTCTGCTACTGCTGCCATCCAGGGCTCTGGCTGGGCTGGCTGGGATTAACCCCTCGAC 440
Qy 480 TAAGAAGCTGGAAGTCAACCAACCGCCCAACGAGGACCTCTGCTTACTCAGATTCCTAT 539
Db 441 CAAACGCTTTGAGATCGCCACCCTCTTCAACGAGGACCTCTCTCTGAGCCACATTCCTAT 500
Qy 540 CATCGAGTTGACATC-TGGGAGCAGCTTCTTACCTTCAAGTACAGAAGCTCAAGCCCTG 598
Db 501 CATCGTGTGATATCTTGGGAGCAGCTTTTACCTCAATATACCTCAACGTCAGAGTTG 560
Qy 599 ACTATCTGCTCTGTTGGTTCGTTATCAACTACAAG 636
Db 561 ATTACTCAACCAATCTGGAGCGTTATCAACTTCGAG 598

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RESULT 9
CF472965
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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CF472965 736 bp mRNA linear EST 05-SEP-2003
RTDS1_12_E11_g1_A015 Drought-stressed loblolly pine roots DSI Pinus
taeda cDNA clone RTDS1_12_E11_A015 5', mRNA sequence.
CF472965
CF472965.1 GI:34490337
EST.
Pinus taeda (loblolly pine)
ORGANISM

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library represents axenically grown fungus ('(FHIG:B)
Axenic plate culture') and a third library represents
axenically grown plants ('(FHIG:C) Axenic plate culture').
Libraries were analyzed in parallel and 3555 (FHIG:A),
3964 (FHIG:B), and 2532 (FHIG:C) high-quality (PHRED 20)
ESTs of >99bp have been deposited. The cDNA libraries were
constructed from total RNA using the SMART cDNA library
Construction kit (#K1051-1, Clontech, Palo Alto, CA, USA)
according to the manufacturer's instructions. Full-length
cDNAs were trimmed by SfiI, fractionated and directionally
ligated into (lambda)Triplex2 arms. The lambda library was
converted to a plasmid library via site-specific
recombination at loxP sites in a Cre+ strain (E. coli
BM25.8). Plasmid clones were randomly collected and
analysed by DNA sequencing using a plasmid-specific
forward primer (P104)."
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 736)

REFERENCE
AUTHORS Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J., Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J., and Neale, D.

TITLE An EST database from drought-stressed loblolly pine (*Pinus taeda*) roots

JOURNAL Unpublished (2003)

COMMENT Other ESTs: RTDS1_12_E11.b1_A015

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: JENREV (CAGGAACAGCTATGACC).

Location/Qualifiers

1..736

/organism="Pinus taeda"

/mol_type="mRNA"

/strain="CCLONES"

/db_xref="taxon:3352"

/clone="RTDS1_12_E11_A015"

/lab_host="DH10B-T1 phage-resistant E. coli"

/clone_lib="drought-stressed loblolly pine roots DS1"

/note="vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from drought-stressed loblolly pine (*Pinus taeda*) roots. Water was withheld from ramet clones until predawn needle water potential reached -1.75 MPa. On day 7 roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Query Match 32.2%; Score 215.4; DB 14; Length 736;
Best Local Similarity 62.8%; Pred. No. 2.1e-47;
Matches 355; Conservative 0; Mismatches 201; Indels 9; Gaps 1;

QY 80 ATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCATCTCCAGGAGA 139

DB 12 ACATTTCGCCCTTGGCGGTATGACTATGATGTCTTCGACCTTACATCTCGAAGCAGA 71

QY 140 TCATGACCCCTTACACACCAAGACCATCATGATTTGTTAAACGGCTCAACGCTGCCG 199

DB 72 TCATGAGCTTCCACACAAAGCATCATCAGACTATGTCAACGCCCTTAACACGCGAA 131

QY 200 AGGAGAGCTACTCGCGCGCTGGCAGGAGGATGTCTTACCAGGTTAAGCTTCAGT 259

DB 132 CCAATGCTTACTCCAGTGTACATCAGCAAAAAGCGAATCGCC-----CTCCAG 182

QY 260 CTGCTCTCAAGTTCAACGGAGGAGACATCAATCACTCTGTCTGGAGAACTTGG 319

DB 183 CTGCTTTGAATTCACCGCGGTGGCCACATTAACCACTCTGTTCTTGGAGAACTTGG 242

QY 320 CTCCTATGATTCGAGGAGGCTACCTCTCTCGAAGGACCTCTCAAGAAAGGCTATCGAGG 379

DB 243 CCCCGCTCCGTTAAAGTGTCGCGGTGTCAATTGCAAGTGGCTCTTCAGCAAGG 302

QY 380 AATCTTTTGGTTCTTTCAGGCGCTTCAAGAGAGAGTTCAACGCTGACACCGCTGCTGCC 439

DB 303 CTATCTCGGACAGTTTCCAGAACTTGAAGGGGAGTTCAAGGCTGCTCGTTGGGCATTC 362

QY 440 AAGGATCCGGATGGGGCTTGGCTTGAACCCCGCTTACTAAGAAAGCTGGAGTCAACCA 499

DB 363 AGGGGTCTGGCTGGTGTGGCTCGGGTTGAACCCCGTCAACCAAGCGCTTGGAGATCACCA 422

QY 500 CGACCCGCCACAGGACCCCTCTCTTACTACACATCTCTATCATCGGAGTTGACATCTGGG 559

DB 423 CCACCCCTTAATCAGGATCCTCTCTTGAATTTGATCCGATCATCGGCTCGCATGTGGG 482

QY 560 AGCAGCGTTTCTACCTTCAGTACAAGAACCTCAAGCCTGACTATCTCGCTGCTGTTTGGT 619

DB 483 AGCAGCGTTTCTACCTTCAGTACAAGAACCTCAAGCCTGACTATCTCGCTGCTGTTTGGT 542

QY 620 CCCTTATCAACTACAAGGAGGCGAGA 644

DB 543 ACCTCATCAACTGGCAGGAGCTGA 567

RESULT 10

CF643518 619 bp mRNA linear EST 02-OCT-2003

LOCUS D91.E07 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA

DEFINITION sequence.

ACCESSION CF643518

VERSION CF643518.1 GI:37411895

KEYWORDS EST.

SOURCE Ustilago maydis

ORGANISM Ustilago maydis

REFERENCE Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes; Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.

AUTHORS Nugent, K.G., Choffe, K. and Saville, B.J.

TITLE Gene Expression during Ustilago maydis Diploid Filamentous Growth: EST Library Creation and Analyses

JOURNAL Unpublished (2003)

COMMENT Contact: Barry J. Saville

Saville Lab

University of Toronto

3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada

Tel: 905 569 4702

Fax: 905 828 3792

Email: bsaville@utoronto.ca

Plate: UTM-UM-D126/7-091-UTM row: 07 column: E

Seq primer: T7 Reverse (5' GAGTAATACGACTCACTATAGG 3')

High quality sequence stop: 619.

FEATURES

Location/Qualifiers

1..619

source /organism="Ustilago maydis"

/mol_type="mRNA"

/strain="FBD12"

/db_xref="taxon:5270"

/cell_type="Mycelia"

/dev_stage="Filamentous diploid"

/clone_lib="Filamentous Forced Diploid"

/note="vector: pSPORT; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."

ORIGIN

Query Match 31.7%; Score 212.4; DB 14; Length 619;
Best Local Similarity 65.3%; Pred. No. 1.2e-46;
Matches 312; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 187 CTCACCGCTCCGAGGAGAGCTACTCGCGCTGTGGCAGGAGGATGTCTTACCAG 246

DB 19 CTCACACCGCTATCAAGGCGCTCAACTCGGCGCATCTCGACACAGAGCTTCGCAAGCAG 78

QY 247 GTTAAGCTTTCAGTCTGCTCTCAAGTTCAACGAGGAGGACACATCAATCACTCTCTGTTTC 306

DB 79 ATTGAGCTCCAGAGCGGCATCAAGTTCAACGCGGTGGCCACATTAACCACTCTGCTCTTC 138

QY 307 TGGAGAACTTGGCTCCCTATGATTCGAGGAGGCTACCCCTCTCTGAGAGGACCTCTCAAG 366

DB 139 TGGAGAACTTGTCTCTCTGCCAGCCAGGCGGTGGACAGCTTCAAGATGGTCCCTTCAAG 198

Plate: IRBD19 row: b column: 07

High quality sequence start: 21

High quality sequence stop: 522.

FEATURES

source
1. .995
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6431706"
/lab_host="DH10B"
/clone_lib="NIH MGC 137"

/note="Organ: pancreas; Vector: pSPORT1; Site 1: SalI; Site 2: NotI; library consists of a pool of clones rearrayed from the following libraries: Melton normalized mixed mouse pancreas 1 NI-MSL1, Amplified Melton mouse islets 1 MSL1-A, and Kaestner ngm3 wt. Clones rearrayed in the laboratory of K. Kaestner (University of Pennsylvania). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 31.5%; Score 211; DB 14; Length 995;
Best Local Similarity 63.2%; Pred. No. 3.9e-46;
Matches 366; Conservative 0; Mismatches 195; Indels 18; Gaps 2;

QY 69 CAGGGCAAGCATACCTGCTGAGTTCCTTACGCTTACGCTTACGCTGCGCTGGAGCCCTCCAT 128
Db 124 CCGGCACAGCAGCTCCAGACCTGCTTACGCTTACGCTTACGCTGCGCTGGAGCCACAT 183
QY 129 CTCGAAGGAGATCATGCCCTTCCACACACAGCACCATCAGACTTATGTTAAAGCCCT 188
Db 184 TAACGGCAGATCATGCAGCTGCACACAGCACCATCGCGCTACGTGAACACCT 243
QY 189 CAACGCTGCCAGGAGAGTACTCGGCGCTGTGGCAAGGAGATGTCTTACCAGGT 248
Db 244 CAACGCCACCGAGAGAAGTACCAAGGCTCTGGCAAGGAGATTTACAACCTCAGGT 303
QY 249 TAAGCTTCAGTGTCTCTCAAGTTCAACGAGGAGGACATCAATCACTCTCTGTCTG 308
Db 304 CGCTCTTCAGCTGCACTGAAGTTCAATGTGGGGACATATTAACACACCTTTCTG 363
QY 309 GAAGAACTTGGCTCCCTATGGATCCGAGGAGGTACCTCTCTGAAGGACCTCTCAAGAA 368
Db 364 GACAACTGAGCCCTAAGGCTGTGGAGAACCA-----AAGGAGTTGCTGGA 414
QY 369 GGCTATCGAGGAATCTTTGGTCTTTTCAGGCGCTTCAAGAGAGTTCAACGCTGACAC 428
Db 415 GGCTATCAAGCGTGACTTTGGTCTTTTGAAGTTTAAAGAGAAGCTGACAGCCGTGC 474
QY 429 CGCTGCTGCCAAGGATCCGAGTGGGCTGGCTTGGCTTGAACCGCTTACTAAGAGCT 488
Db 475 TGTGGAGTCCAGGTTCAAGTTCAGCTGGGCTGGCTTGGCTTCAAGAGGAGTGCCTT 534
QY 489 GGAAGTCACACGACCGCCCAACGAGGCCCTCTGC-----TTACTCACATTCCTAT 539
Db 535 ACAGATTGCTGCTGCTCTAATCAGGACCCATTCGAAGGACACAGGCCCTTATTCGCT 594
QY 540 CATCGGAGTTGAATCTGGGAGACGCTTTCTACTCTTCAAGTACAGAGCTCAAGCTGA 599
Db 595 GCTGGGAGTTGACGTGTGGGAGCAGCTTACTTACCTTCAATATATAAAGCTGACACCTGA 654
QY 600 CTATCTCGTCTGCTTTGGTCCGTTATCACTACAAGGA 638
Db 655 CTAICTGAAAGCTATTTGGAATGTAATCACTGGAGNA 693

RESULT 13

BU060841

LOCUS

DEFINITION

Fgr-C_1_k18_T3 Carbon-starved mycelia Gibberella zeae cDNA, mRNA

sequence.

BU060841

ACCESSION

VERSION

BU060841.1 GI:22501130

KEYWORDS

746 bp mRNA linear EST 26-AUG-2002

SOURCE
ORGANISM

Gibberella zeae
Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE

1 (bases 1 to 746)

AUTHORS

Trail, F., Xu, J.-R., San Miguel, P., Haigren, R.G. and Kistler, H.C.

TITLE

Analysis of expressed sequence tags from Gibberella zeae (anamorph

Fusarium graminearum)

JOURNAL

Fungal Genet. Biol. 38 (2), 187-197 (2003)

MEDLINE

22508120

PUBMED

12620255

COMMENT

Contact: Frances Trail

Department of Plant Biology

Michigan State University

East Lansing, MI 48824, USA

Tel: 517 432 2939

Fax: 517 353 1926

Email: trail@msu.edu

Plate: 1 row: K column: 18.

Location/Qualifiers

1. .746

/organism="Gibberella zeae"

/mol_type="mRNA"

/strain="NRRL 31084"

/db_xref="taxon:5518"

/clone_lib="Carbon-starved mycelia"

/note="Vector: Uni-ZapII; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 31.5%; Score 210.8; DB 13; Length 746;

Best Local Similarity 61.9%; Pred. No. 3.7e-46;

Matches 351; Conservative 0; Mismatches 213; Indels 3; Gaps 1;

QY 68 TCAGGGCAAGCATACCTGCTGAGTTCCTTACGCTTACGCTGCGCTGGAGCCCTCCA 127

Db 126 TCCGCGGCAAGGCCATCTCCCGATCTTCCCTTACGACTATGGCGTCTTGGAGCCCTACA 185

QY 128 TCTCCAAGGAGATCATGACCTTCAACACACCAAGCACCATCAGACTTATGTTAAAGGCC 187

Db 186 TCTCTGGCAGATCTGGAGCTTCAACATCCCAAGCACCACAGACTAGTTACCGGCT 245

QY 188 TCAACGCTGCCGAGGAGAGTACTCGGCGCTGTGGCAAGGAGGATGTCTTACCCAGG 247

Db 246 TCAACAGCTACCGACGCCATCGCGAGCCCAACCAAGGCGAGCCCAAGGCTGCTG 305

QY 248 TTAAGCTTCAGTCTGCTTCAAGTTCAACGAGGAGGAGACATCAATCACTCTGTGTTCT 307

Db 306 CCGCTCAGGCTCTCTCTCAACTTCCACGCGGTGGTCACTCAACCTTCCCTCTTCT 365

QY 308 GGAAGAACTTGGCTTCCCTATGGATCCGAGGAGGCTACCTCTCTGAAGGACCTCTCAAGA 367

Db 366 GGGAGAACCTTGTCTCCCAAGGTAAGGCGGTGGTGGAGCCCGAGGGCAAGCTTCTGA 425

QY 368 AGGCTATCGAGGAATCTTTGGTCTTTTCAGGCGCTTCAAGAGAGAGTTCAACGCTGACA 427

Db 426 CTTCCATCAACGAGGACTTTTGGCTCTTTCAGGCGCTTCAAGAGAGAGAGCAACGCTACCC 485

QY 428 CCGTCTGTCTCAAGGATCGGATGGGCTGGCTTGGCTTGAACCCGCTTACTAAGAGC 487

Db 486 TCGCGGTATCCAGGCTCGGCTGGGCTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 545

QY 488 TGGAGTCAACACGAGCCCAACGAGGACCTCTGTCTTACTTCACTT---CCTATCATCG 544

Db 546 TGTCCATCTTATCCCGACCCCAACGAGACCCCGTCCCGGTACCTTGGAGCCCTCTCTCG 605

QY 545 GAGTTGATCTGGGAGCAGCTTTTCTACCTTCAGTACAAGAGAGCTCAAGCTGACTATC 604

Db 606 GCATTGACGCTGNGAGCAGCGCTTACTTACTTCACTTCACTTCACTTCACTTCACTTCACT 665

QY 605 TCGCTGCTGTTGGTCCGTTATCACT 631

Db 666 TCAGGCCATCTGGGAGCTCATCACT 692

RESULT 14
CD488011 577 bp mRNA linear EST 29-AUG-2003
LOCUS T03_D04 Teliospore Ustilago maydis cDNA 5', mRNA sequence.
DEFINITION CD488011
ACCESSION CD488011
VERSION CD488011.1 GI:34330509
KEYWORDS EST.
SOURCE Ustilago maydis
ORGANISM Ustilago maydis
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes; Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
REFERENCE 1 (bases 1 to 577)
AUTHORS Sacadura,N.T. and Saville,B.J.
TITLE Gene expression and EST analyses of Ustilago maydis germinating teliospores
JOURNAL Fungal Genet. Biol. 40 (1), 47-64 (2003)
MEDLINE 22829673
PubMed 12948513
COMMENT Contact: Barry J. Saville
Saville Lab
University of Toronto
3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
Tel: 905 569 4702
Fax: 905 828 3792
Email: bsaville@utoronto.ca
Seq primer: M13 reverse primer (5' AACAGCTATGACCATGTTCA 3').
FEATURES
source
1..577
/organism="Ustilago maydis"
/mol_type="mRNA"
/strain="FBI/FB2"
/db_xref="taxon:5270"
/cell_type="Teliospore"
/dev_stage="Germinating teliospore"
/lab_host="E. coli"
/clone_lib="Teliospore"
/note="Vector: pDNR-LIB; Site 1: SfiIA; Site 2: SfiIB; mRNA was extracted from germinating teliospores. cDNA was amplified by PCR and unidirectionally cloned into pDNR-LIB plasmid, with the use of Clontech's Creator SMART cDNA Library Construction Kit."

ORIGIN
Query Match 31.4%; Score 210.4; DB 14; Length 577;
Best Local Similarity 65.1%; Pred. No. 4.1e-46;
Matches 324; Conservative 0; Mismatches 173; Indels 1; Gaps 1;
QY 28 GTGCTAGACAGACTTCGTCGCTCCTGCTGCTTTCCAGATCAGGCGAAGCATCCCTG 87
DB 78 GCCTGTCGCGCAGTTTGTGCGCTCTGCGCTGCGCGCTGCGAGCAAGCACACGCTT 137
QY 88 CTTGAGCTTCCTAGGCTTAGATGCGCTGAGCGCTCCATCTCCAGGAGATCATGACC 147
DB 138 CCCGACCTGGCTTTGAGTACGGTGCACTCGAGCGCGCCATTCATCAAGATCATGAG 197
QY 148 CTTACACACCAAGCAGCATCAGACTTATGTTAACGGCCCTCAAGCTGCGGAGGAGAGC 207
DB 198 CTACACACACCAAGCATCAGACCTATGTCAACGCTCTCAACCGCGGAGAGAGAGC 257
QY 208 TACTCGGCGCTGGGCAAGGAGATGTGCTTACCCAGGTTAAGCTTCAGTCTGCTCTC 267
DB 258 CTCTCTGAAGGATCCACAAAGAGACGCTCAGGTGCGCAATCGCTCTTCAGAAAGCGATC 317
QY 268 AAGTTCAAGGAGGAGACACATCAATCACTCTGTTCTGGAAGACTTGCTGCTCCCTAT 327
DB 318 AACTTTAAGCGGTGTGCATCAACCACTCTCTTTGGGAGATCTGGCCCCGAG 377
QY 328 GGATCCGAGGAGGTACCTCTCTGAAGGACCTCTCAAGAGGCTTATCGAGGAATCTTTT 387
DB 378 AAGATGCGGTGTGAGTTGAGCAGCGGCGCTCTCAAGGACGCTATCGACCGAGACTTT 437
QY 388 GGTCTTTCGAGGCGCTTCAGAGAGTTCACGCTGACCGCTGCTGTCTCAAGGATCC 447

DB 438 GGTGGTTTGGACCAGCTCAAGTCCAAAGTTCAATGCTCAGATCGCTGCCATCCAGGTTCC 497
QY 448 -CGATGGGGCTGGCTTGAACCCGCTTACTTAAGAGCTGGAAGTCAACACGACCGC 506
DB 498 NGTTTGGGNTGGCTCGGCTACACCCGAGACCAAGAGCTCGACATNGTCACTACCGC 557
QY 507 CAACGAGGACCTCTGCT 524
DB 558 CAACGAGGACCTCTGCT 575
AT002967 468 bp mRNA linear EST 25-MAR-2002
AT002967 POSLM01 Pleurotus ostreatus cDNA clone 460LM, mRNA
sequence.
ACCESSION AT002967
VERSION AT002967
KEYWORDS EST.
SOURCE AT002967.1 GI:6934694
ORGANISM Pleurotus ostreatus (oyster mushroom)
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Agaricales; Pleurotaceae; Pleurotus.
REFERENCE 1 (bases 1 to 468)
AUTHORS Lee,S.H., Kim,B.G., Kim,K.J., Lee,J.S., Yun,D.W., Hahn,J.H., Kim,G.H., Lee,K.H., Suh,D.S., Kwon,S.T., Lee,C.S. and Yoo,Y.B.
TITLE Comparative Analysis of Sequences Expressed during the Liquid-Cultured Mycelia and Fruit Body Stages of Pleurotus ostreatus
JOURNAL Fungal Genet. Biol. 35 (2), 115-134 (2002)
MEDLINE 21838665
PubMed 11848675
COMMENT Contact: Kim BG
Division of applied microbiology
National Institute of Agricultural Science and Technology (NIATST)
Seodundong, Suwon, Kyung-gi 441-707, South Korea
Email: bgkim@niatst.go.kr
Submitted through BRIC(Biological Research Information Center) of Korea
URL: http://bric.postech.ac.kr/.
Location/Qualifiers
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/organism="Pleurotus ostreatus"
/mol_type="mRNA"
/cultivar="ASI 2029"
/db_xref="taxon:5322"
/clone="460LM"
/dev_stage="shaking liquid cultured mycelia"
/lab_host="E.coli"
/clone_lib="PSLM01"
/note="Vector: lambda Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI; average insert size:1000 bp;initial pfu:5 x 10⁷
Library information:isolation of total RNA from the mycelia incubated in shaking liquid MCM media at 30 deg C"

ORIGIN
Query Match 31.3%; Score 209.6; DB 9; Length 468;
Best Local Similarity 72.9%; Pred. No. 6e-46;
Matches 283; Conservative 0; Mismatches 104; Indels 1; Gaps 1;
QY 276 CGGAGGAGGACACATCACTCTCTGTTCTGGAAGAACTGGCTCCCTATGGATCGA 335
DB 1 CGTGGTGGTCCATCAACCACTCTCTCTCTGGAAGAACTTGCACCTGCTAGCGGTGA 60
QY 336 GGAGCTTACCTCTCTGAGGACCTCTCAAGAGCTATCGAGGAATCTTTGTTCTTT 395
DB 61 CGGAGGCAAACTTCAGATGGCCCTTGAAGCAAGCCATCGAAGAGACTTTGGACCGT 120
QY 396 CGAGGCTTCAAGAGAGTTCACGCTGACACCGCTCTCTCCAAAGATCCGATGGG 455
DB 121 CGAAGATTCAGAAAAAGTTCAACACCAACCATGCTG-TGTCCAAGCGATGCTGGG 179


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QY 456 CTGGCTTGGCTTGAAACCGCTTACTAAGAAGCTGGAAGTCACACAGACCGCCACACAGGA 515
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 180 CTGGCTTGGATTCAATCCACCAACAAGAGCTCGAGTCACACAGACCGCCACACAGGA 239
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QY 516 CCCTCTGCTTACTACACATTCTATCATCGGAGTTGACATCTGGAGGACGCTTTCTACCT 575
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 240 CCCCTTGATAACTCACGCGCGGATCATCGGTGTTGACATTTGGGAACATGCCCTTCTACCT 299
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 576 TCAGTACAGAAGCTCAAGCTGACTATCTCGCTGCTGTTGGTCCGTTATCAACTACAA 635
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 300 CCAATACAGAAGCTGAAGCTGATTACCTCAATGCTATCTGGAAACGTTATCAACTTCAA 359
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 636 GGAGGCAGAGCGCCGATTGCGAGGCTGCT 663
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Search completed: April 1, 2004, 21:52:38
Job time : 1732 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 12:34:16 ; Search time 233.318 Seconds
(without alignments)
10723.022 Million cell updates/sec

Title: US-09-727-855B-4

Perfect score: 669

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Gapop 10.0 , Gapext 1.0

Searched: 2465228 seqs, 1869859620 residues

Total number of hits satisfying chosen parameters: 4930456

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications NA:*
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 - 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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 - 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
 - 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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 - 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
 - 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	316.6	47.3	597	9	US-09-727-855B-6
3	252	37.7	728	14	US-10-109-670-3
4	250.6	37.5	812	14	US-10-109-670-4
5	230.6	33.0	630	14	US-10-109-670-29
6	205	30.6	1492	9	US-09-917-800A-1627
7	202.8	30.3	987	12	US-10-424-599-90405
8	199.6	29.8	2217	12	US-10-424-599-90403
9	197.8	29.6	972	13	US-10-044-090-836
10	197.8	29.6	996	14	US-10-198-846-13503
11	197.8	29.6	1026	9	US-09-954-456-1822
12	197.8	29.6	1026	12	US-10-342-887-509
13	197.8	29.6	1026	12	US-10-342-887-1905
14	197.8	29.6	2825	14	US-10-198-846-13787
15	188	28.1	817	9	US-09-770-445-745

16	185.4	27.7	894	14	US-10-247-671-122	Sequence 122, App	
17	184.6	27.6	1067	10	US-09-971-439B-22	Sequence 22, Appl	
18	182.2	27.2	1295	15	US-10-310-154-294	Sequence 294, App	
19	178	26.6	2208	13	US-10-044-090-709	Sequence 709, App	
20	170.8	25.5	732	14	US-10-230-331-9	Sequence 9, Appl	
21	151.4	22.6	3632	9	US-09-727-855B-1	Sequence 1, Appl	
22	142	21.2	371	14	US-10-109-670-25	Sequence 25, Appl	
23	139	20.8	1143	9	US-09-818-564-1	Sequence 1, Appl	
24	136	20.3	477	10	US-09-911-904-182	Sequence 182, Appl	
25	134.6	20.1	1230025	15	US-10-289-762-1	Sequence 1, Appl	
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33	111	16.6	344	10	US-09-918-995-24298	Sequence 24298, A	
34	107	16.0	325	9	US-09-993-333-11	Sequence 11, Appl	
35	106	15.8	419	9	US-09-960-352-4975	Sequence 4975, Ap	
36	104.8	15.7	429	9	US-09-960-352-13978	Sequence 13978, A	
37	102.6	15.3	414	9	US-09-960-352-731	Sequence 731, App	
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39	100.4	15.0	398	9	US-09-960-352-14457	Sequence 14457, A	
c	40	98.6	14.7	456	9	US-09-960-352-12575	Sequence 12575, A
c	41	98	14.6	425	9	US-09-960-352-5493	Sequence 5493, Ap
42	93.8	14.0	376	9	US-09-920-455-67	Sequence 67, Appl	
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c	44	90.6	13.5	413	9	US-09-960-352-5724	Sequence 5724, Ap
c	45	90.6	13.5	417	9	US-09-960-352-12085	Sequence 12085, A

ALIGNMENTS

RESULT 1
US-09-727-855B-4
; Sequence 4, Application US/09727855B
; Patent No. US20020168703A1
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUL
; TITLE OF INVENTION: MATERIALS THEREOF
; FILE REFERENCE: C38435/111694
; CURRENT APPLICATION NUMBER: US/09/727,855B
; CURRENT FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Phaffia rhodozyma
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(666)
; OTHER INFORMATION: n or X = A, C, G or T
US-09-727-855B-4

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Best Local Similarity 100.0%; Pred. No. 2.6e-213; Indels 0; Gaps 0;
Matches 669; Conservative 0; Mismatches 0;

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Db	61	TTCCAGATAGGGGAAAGCATACCCCTGCTGAGCTTCCTTACGTTACGATGACGCTGGAG	120
Qy	121	CCCTCCATCTCCAGGAGATCATGACCTTCACCAACCAACCATCAGACTTAATGTT	180

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 Qy 658 GCTGCTCTC 666
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US-09-917-800A-1627
 ; Sequence 1627, Application US/09917800A
 ; Patent No. US20020119462A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mendrick, Donna
 ; APPLICANT: Porter, Mark
 ; APPLICANT: Johnson, Kory
 ; APPLICANT: Castle, Arthur
 ; APPLICANT: Elashoff, Michael
 ; APPLICANT: Gene Logic, Inc.
 ; TITLE OF INVENTION: Molecular Toxicology Modeling

; FILE REFERENCE: 44321-5038-US
 ; CURRENT APPLICATION NUMBER: US/09/917,800A
 ; CURRENT FILING DATE: 2001-07-31
 ; PRIOR APPLICATION NUMBER: US 60/222,040
 ; PRIOR FILING DATE: 2000-07-31
 ; PRIOR APPLICATION NUMBER: US 60/222,880
 ; PRIOR FILING DATE: 2000-11-02
 ; PRIOR APPLICATION NUMBER: US 60/290,029
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: US 60/290,645
 ; PRIOR FILING DATE: 2001-05-15
 ; PRIOR APPLICATION NUMBER: US 60/292,336
 ; PRIOR FILING DATE: 2001-05-22
 ; PRIOR APPLICATION NUMBER: US 60/295,798
 ; PRIOR FILING DATE: 2001-06-06
 ; PRIOR APPLICATION NUMBER: US 60/297,457
 ; PRIOR FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/298,884
 ; PRIOR FILING DATE: 2001-06-19
 ; PRIOR APPLICATION NUMBER: US 60/303,459
 ; PRIOR FILING DATE: 2001-07-09
 ; NUMBER OF SEQ ID NOS: 1740
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1627
 ; LENGTH: 1492
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; FEATURE:
 ; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_017051
 US-09-917-800A-1627

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 Qy 189 CAAAGCTGCGAGGAGAGTACTCGCCGCTGCGAGGAGGATGCTTACCCAGT 248

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 Qy 249 TAAGCTTCAGTCTGCTCTCAAGTTCAACGAGGAGGACACATCAATCACTCTCTGTTCTG 308
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 Qy 369 GGTATTCAGAGAAATCTTTTGGTCTTTTCGAGGCTTCAAGAGAGAGTTCAGCGTGACAC 428
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 Qy 429 CGCTGCTGTCCAAGGATCGGATGGGCTGGCTTGGCTTGAACCCGCTTACTAAGAAGCT 488
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 Qy 540 CATCGAGTTGACATCTGGGAGCAGCTTTCTACCTTCAGTACAGAGAGCTCAAGCTCA 599
 Db 605 GCTGGGATTGATGTGGGAGCAGCTTACTATCTTCAATATAAAACGTCAGACCTGA 664
 Qy 600 CTATCTGCTGCTGTTTGGTCCGCTTATCAACTACAAGGAGG 640
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RESULT 7

US-10-424-599-90405/c
 ; Sequence 90405, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 90405
 ; LENGTH: 987
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MBT3847_52648C.1
 US-10-424-599-90405

Query Match 30.3%; Score 202.8; DB 12; Length 987;
 Best Local Similarity 61.1%; Pred. No. 4e-57;
 Matches 352; Conservative 0; Mismatches 212; Indels 12; Gaps 1;
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 Db 746 CATCATGAGCTGCACCCAGGAGCAGCACCAGACTTATACCACTACCAAGGC 687
 Qy 198 CGAGAGAGCTACTCGGCGCTGTGGGCAAGAGAGATGCTTACCAGTTAAGCTTCA 257
 Db 686 CTTGAGCAGCTTCCAAAGAGCGCCATCGCCAAAGAGATTCTCCCGCGTGTAAAGTCCA 627
 Qy 258 GTCTCTCTCAAGTTCAAGGAGGAGGACACATCAATCACTCTCTGTTCTGGAAGACTT 317
 Db 626 GGGCGCCATCAAGTTCAACGCGGAGGATCATGTCAACCAATCTATTTCTGAAAAATCT 567

QY 249 TAAGCTTCAGTCTGCTCTCAAGTTCAACGAGGAGGACACATCAATCACTCTCTGTTCTG 308
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 QY 309 GAAGAACTTGGCTCCCTATGAGTCCGAGGAGGCTACCTCTCTGAGAGCACTCTCAAGAA 368
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RESULT 12

US-10-342-887-509
 ; Sequence 509, Application US/10342887
 ; Publication No. US20040058340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dai, Hongyue
 ; APPLICANT: He, Yudong
 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Mao, Mao
 ; APPLICANT: Roberts, Christopher J.
 ; APPLICANT: Van 't Veer, Laura Johanna
 ; APPLICANT: Van de Vijver, Marc J.
 ; APPLICANT: Bernards, Rene
 ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
 ; FILE REFERENCE: 9301-188-999
 ; CURRENT APPLICATION NUMBER: US/10/342,887
 ; PRIOR FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: 60/298,918
 ; PRIOR FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: 60/380,710
 ; PRIOR FILING DATE: 2002-05-14
 ; PRIOR APPLICATION NUMBER: 10/172,118
 ; PRIOR FILING DATE: 2002-06-14
 ; NUMBER OF SEQ ID NOS: 2699
 ; SEQ ID NO 509
 ; LENGTH: 1026
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-342-887-509

Query Match 29.6%; Score 197.8; DB 12; Length 1026;
 Best Local Similarity 60.9%; Pred. No. 1.9e-55;
 Matches 366; Conservative 0; Mismatches 217; Indels 18; Gaps 2;
 QY 69 CAGGGCAAGCATACCTGCTGAGTCTCTTACGCTTAGCATGCTGAGGCGCTCCAT 128
 Db 70 CAGGGCAAGCAGAGCTCCCGACCTTACGCTTAGCATGAGGCGCTCCAT 129
 QY 129 CTCCAAGGAGATCATGACCTTCCACCACCAAGCAGCATCATGTTTAAAGCGCT 188

Db 130 CAACGCGAGATCATGAGCTGCACCAACAGCAAGCAACACCGCGCTACGTGAACAACT 189
 QY 189 CAACGCTGCCAGGAGAGTACTCGCGCTGTGGCAGGAGGATGTCTTACCAGCT 248
 Db 190 GAACGTCACCGAGGAGAGTACCGAGGCGGTGTGGCAAGGAGAGTGTACAGCCAGAT 249
 QY 249 TAAGCTTCAGTCTGCTCTCAAGTTCAACGAGGAGGACACATCAATCACTCTCTGTTCTG 308
 Db 250 AGCTCTTCAGCTCTGACTGAAGTTCAATGGTGTGTATATCAATCATAGCATTTTCTG 309
 QY 309 GAAGAACTTGGCTCCCTATGAGTCCGAGGAGGCTACCTCTCTGAGAGCACTCTCAAGAA 368
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 QY 369 GCCTATCGAGGAATCTTTTGGTCTTTTCGAGGCTTCAAGAAAGTTCAACGCTGACAC 428
 Db 361 AGCCATCAAACTGGACTTTGGTCTTTGACAAAGTTTAAAGGAGAACTGACGGCTGCATC 420
 QY 429 CGCTGCTGTCGAAGATCCGAGTGGGCTGGCTTGAACCCGCTTACTAAGAGCT 488
 Db 421 TGTGGTGTCCAAGCTCAGTTGGGTTGGCTTGTTCATTAAGAAAGGGGACATTT 480
 QY 489 GGAAGTTCACACGACCGCAACAGGACCTCTGC-----TTACTCACATTCCTAT 539
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 QY 540 CATCGAGTTGACATCTGGAGCAGCTTTTACCTTTCAGTACAGAAAGCTCAAGCTGA 599
 Db 541 GCTGGGATTTGATGTGTGGGAGCAGCTTTACTACCTTCAGTATAAAATGTTCAGGCTGA 600
 QY 600 CTATCTCGCTGCTGTTTGGTTCGTTTATCAACTACAGGAGGAGGAGGCGGCTTGCAGGC 659
 Db 601 TTATCTAAAGCTATTGGAATGTAATCAACTGGGAGAAATGTAACCTGAAAGATACATGCG 660
 QY 660 T 660
 Db 661 T 661

RESULT 13

US-10-342-887-1905
 ; Sequence 1905, Application US/10342887
 ; Publication No. US20040058340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dai, Hongyue
 ; APPLICANT: He, Yudong
 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Mao, Mao
 ; APPLICANT: Roberts, Christopher J.
 ; APPLICANT: Van 't Veer, Laura Johanna
 ; APPLICANT: Van de Vijver, Marc J.
 ; APPLICANT: Bernards, Rene
 ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
 ; FILE REFERENCE: 9301-188-999
 ; CURRENT APPLICATION NUMBER: US/10/342,887
 ; PRIOR FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: 60/298,918
 ; PRIOR FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: 60/380,710
 ; PRIOR FILING DATE: 2002-05-14
 ; PRIOR APPLICATION NUMBER: 10/172,118
 ; PRIOR FILING DATE: 2002-06-14
 ; NUMBER OF SEQ ID NOS: 2699
 ; SEQ ID NO 1905
 ; LENGTH: 1026
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-342-887-1905

Query Match 29.6%; Score 197.8; DB 12; Length 1026;
 Best Local Similarity 60.9%; Pred. No. 1.9e-55;
 Matches 366; Conservative 0; Mismatches 217; Indels 18; Gaps 2;

QY 69 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 128
 |||||
 DB 70 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 129
 |||||
 QY 129 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 188
 |||||
 DB 130 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 189
 |||||
 QY 189 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 248
 |||||
 DB 190 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 249
 |||||
 QY 249 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 308
 |||||
 DB 250 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 309
 |||||
 QY 309 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 368
 |||||
 DB 310 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 369
 |||||
 QY 369 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 428
 |||||
 DB 361 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 429
 |||||
 QY 429 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 488
 |||||
 DB 421 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 489
 |||||
 QY 489 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 539
 |||||
 DB 481 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 540
 |||||
 QY 540 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 599
 |||||
 DB 541 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 600
 |||||
 QY 600 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 659
 |||||
 DB 601 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 660
 |||||
 QY 660 T 660
 DB 661 T 661

RESULT 14

US-10-846-13787
 ; Sequence 13787, Application US/10198846
 ; Publication No. US2003009974A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lillie, James
 ; APPLICANT: Xu, Yongyao
 ; APPLICANT: Wang, Youzhen
 ; APPLICANT: Steinmann, Kathleen
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
 ; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; FILE REFERENCE: MRI-049
 ; CURRENT APPLICATION NUMBER: US/10198,846
 ; CURRENT FILING DATE: 2002-07-18
 ; PRIOR APPLICATION NUMBER: 60/306,220
 ; PRIOR FILING DATE: 2001-07-18
 ; NUMBER OF SEQ ID NOS: 14084
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13787
 ; LENGTH: 2825
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-846-13787

Query Match 29.6%; Score 197.8; DB 14; Length 2825;
 Best Local Similarity 60.9%; Pred. No. 2.9e-55;

Matches 366; Conservative 0; Mismatches 217; Indels 18; Gaps 2;
 QY 69 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 128
 |||||
 DB 215 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 274
 |||||
 QY 129 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 188
 |||||
 DB 275 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 334
 |||||
 QY 189 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 248
 |||||
 DB 335 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 394
 |||||
 QY 249 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 308
 |||||
 DB 395 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 454
 |||||
 QY 309 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 368
 |||||
 DB 455 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 505
 |||||
 QY 369 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 428
 |||||
 DB 506 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 565
 |||||
 QY 429 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 488
 |||||
 DB 566 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 625
 |||||
 QY 489 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 539
 |||||
 DB 626 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 685
 |||||
 QY 540 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 599
 |||||
 DB 686 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 745
 |||||
 QY 600 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 659
 |||||
 DB 746 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 805
 |||||
 QY 660 T 660
 DB 806 T 806

RESULT 15

US-09-770-445-745
 ; Sequence 745, Application US/09770445
 ; Patent No. US20020023281A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gorlach, Jorn
 ; APPLICANT: An, Yong-Qiang
 ; APPLICANT: Hamilton, Carol M.
 ; APPLICANT: Price, Jennifer L.
 ; APPLICANT: Raines, Tracy M.
 ; APPLICANT: Yu, Yang
 ; APPLICANT: Rameaka, Joshua G.
 ; APPLICANT: Page, Amy
 ; APPLICANT: Matthew, Abraham V.
 ; APPLICANT: Ledford, Brooke L.
 ; APPLICANT: Woessner, Jeffrey P.
 ; APPLICANT: Haas, William David
 ; APPLICANT: Kricker, Carlos A.
 ; APPLICANT: Slader, Ted
 ; APPLICANT: Davis, Keith R.
 ; APPLICANT: Allen, Keith
 ; APPLICANT: Hoffman, Neil
 ; APPLICANT: Hurbán, Patrick
 ; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
 ; TITLE OF INVENTION: thaliana

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	692	50.0	224	2	AAw29771	Malassezi
2	668.5	58.0	206	2	AAw29770	AAw29770 Malassezi
3	634.5	55.0	222	7	ADD45869	Rat Prote
4	623	54.0	222	2	AAw98170	Human rat
5	623	54.0	222	3	AAw08204	Amino aci
6	621	53.9	222	2	AAw44801	MnSOD cDN
7	621	53.9	222	2	AAw90713	Human man
8	621	53.9	222	2	AAw00018	Human man
9	621	53.9	222	2	AAw98169	Human rat
10	620	53.8	222	2	AAw98175	Human man
11	619	53.7	222	1	AAp71701	Recombina
12	619	53.7	223	1	AAw80551	Human man
13	618	53.6	222	2	AAw00453	Human man
14	618	53.6	222	2	AAw98171	Human man
15	618	53.6	222	2	AAw98174	Human man
16	618	53.6	222	3	AAw98173	Human man
17	618	53.6	222	3	AAw08205	Q143N mod
18	617	53.5	222	2	AAw61337	Human man
19	617	53.5	222	2	AAw96317	Human man
20	617	53.5	222	2	AAw82446	Human mSO
21	617	53.5	222	2	AAw98172	Human man
22	617	53.5	222	3	AAw08206	A modifie
23	616	53.4	222	2	AAw98176	Human man
24	616	53.4	222	5	AAw79798	Human man
25	616	53.4	222	5	AAw07330	Human man

```
SQ Sequence 224 AA;
Query Match 60.0%; Score 692; DB 2; Length 224;
Best Local Similarity 59.3%; Pred. No. 5.4e-66;
Matches 128; Conservative 31; Mismatches 53; Indels 4; Gaps 1;
QY 11 SROTFFVAP---AAFOIRAKHTLPPLPYADALEPSISKEIMTLHHTKHQTYVNGLNAA 66
D 6 TRRAAAPLANAAQMGVETKTLPLPYDYGALPEAISGEIMETHYKHKHTYVNNLNA 65
QY 67 EESYSAAVGKBDVLTQVKLSALKFNGGGHINHSFLWKNLAPYGSSEATLSEGPLKKAIE 126
D 66 EDKLIDALPOQSPLGEIAQLNAIKFNGGGHINHSFLWKNLAPYKGGGELDSGELRSAID 125
QY 127 ESFGSFEAFKKENADTAAVOGSGWGLGNPLTKKLEVTITANQDPLLTTHPIIIGVDIW 186
D 126 RDFSVDAMKEFNAALAGIQSGSGWGLGNPLTKKLEVTITANQDPLLTTHPIIIGVDIW 185
QY 187 EHAFYLOYNKVPDYLAAVWSVINYKEAEARLQAL 222
D 186 EHAFYLOYNKVKADYFKAIWTVINFEAEKRLKEAL 221

RESULT 2
AAW29770
ID AAW29770 standard; protein; 206 AA.
XX
AC AAW29770;
XX
DT 27-AUG-2003 (revised)
DT 23-FEB-1998 (first entry)
XX
DE Malassezia fungus MF-3 antigenic protein.
XX
KW Malassezia; fungus; antigenic; human; IgE; immunoglobulin E; antibody;
KW allergy; antigen.
XX
OS Malassezia.
XX
PN WO9721817-A1.
XX
PD 19-JUN-1997.
XX
PF 10-DEC-1996; 96WO-JP003602.
XX
PR 12-DEC-1995; 95JP-00346627.
XX
PR 05-SEP-1996; 96JP-00257612.
XX
PR 05-SEP-1996; 96JP-00257613.
XX
PA (TAKI ) TAKARA SHUZO CO LTD.
XX
PI Takesako K, Okado T, Yagihara T, Kuroda M, Onishi Y, Kato I;
PI Akiyama K, Yasueda H, Yamaguchi H;
XX
WPI; 1997-332788/30.
D N-PSDB; AAT85876.
PT Antigenic proteins from the fungus Malassezia - bind to IgE antibodies
PT present in patients with Malassezia allergies, useful for diagnosis,
PT treatment and prevention of such conditions.
XX
PS Claim 36; Page 83-84; 162pp; Japanese.
XX
CC The present sequence represents a specifically claimed antigenic protein
CC isolated from the fungus Malassezia. The antigenic protein can bind to
CC IgE antibodies present in patients with allergic conditions. Antigenic
CC proteins, peptides and nucleic acids from the fungus Malassezia can be
CC used in the diagnosis, treatment and prevention of allergic conditions
CC due to Malassezia organisms (such as M.furfur, M. sympodialis and
CC M.pachydermatitis). (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 206 AA;
Query Match 58.0%; Score 668.5; DB 2; Length 206;
Best Local Similarity 63.1%; Pred. No. 1.7e-63;
Matches 123; Conservative 24; Mismatches 47; Indels 1; Gaps 1;
QY 23 IRAKHTLPPLPYADALEPSISKEIMTLHHTKHQTYVNGLNAAEESYSAAVGKEDVLTQ 82
D 3 VMTYTLPLPLPYADALEPFIKSEIMTVHDDKHQTYVNNLNAAEKAYAEATAANDVLKQ 62
QY 83 VKLOSALKFNGGGHINHSFLWKNLAPYGSSEATLSEGPLKKAIEBSFGSFEAFKKKFNAD 142
D 63 IQLSALKFNGGGHINHSFLWKNLAPQSEGGQLNDGPLKQALIEQEGDFEFKTTNTK 122
QY 143 TAAVQSGSGWGLGNPLTKKLEVTITANQDPLLTTHPIIIGVDIWEHAFYLOYNKVPDY 202
D 123 AAGIQSGSGWGLGVAP-TGNLDLVVAKDQDPLTTHHPVIGWDGWEHAWYLOYNKDKASYL 181
QY 203 AAVWSVINYKEAEAR 217
D 182 KAWNVVNVNAEAKR 196

RESULT 3
ADD45869
ID ADD45869 standard; protein; 222 AA.
XX
AC ADD45869;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein CAA39937, SEQ ID NO 11539.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
XX
PR 01-NOV-2001; 2001US-0346382P.
XX
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO ) GEN HOSPITAL CORP.
XX
PA (FARB ) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
WPI; 2003-268312/26.
D GENBANK, CAA39937.
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
```

method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 222 AA;

Query Match 55.0%; Score 634.5; DB 7; Length 222;
 Best Local Similarity 55.4%; Pred. No. 8.7e-60;
 Matches 123; Conservative 30; Mismatches 58; Indels 11; Gaps 4;
 QY 1 MSVRASLSVSRQTFFVAPAAFI--RAKHTLPYAYDALEPSISKEIMTLHHTKHQT 58
 Db 1 MLCRAACSGRR---LGPRASTAGSRKHSPLDLYDGALEPHINAQIMQLHRSKHAT 57
 QY 59 YVNGLNAAEESYGAAYGKEDVLTQVLSALKFNGGGHINHSFWKNLAPYGSSEATLSE 118
 Db 58 YVNNLVNTEEKYHEALAKGDVTTQVALQPALKFNNGGGHINHSIFWNLSPKGGGE---PK 114
 QY 119 GPLKKAIESFGFEAFKPKFNADTAAGVSGGWMGLNPLTKKLEVTNTANODPL---L 175
 Db 115 GELLEAKRDFSGFEKFKELTAVSVGVQSGGWMGLFNKEQRLQIAACSNQDPLQGT 174
 QY 176 THPIIGVDIWEHAFYLYQKNVKPDYLAAVWSVINYKEAEAR 217
 Db 175 GLIPLGIDWEHAYLYQKNVRPDYLYKAIWNVINWENVSQR 216

RESULT 4

AAW98170
 ID AAW98170 standard; protein; 222 AA.

XX AAW98170;

XX 05-JUL-1999 (first entry)

XX Human native manganese superoxide dismutase.

XX Superoxide dismutase; MnSOD; SOD; human; protein engineering;
 KW enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
 KW inflammation; reperfusion injury; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..24
 FT /note= "signal peptide"
 FT Protein 25..222
 FT /note= "mature protein"
 FT Active-site 50
 FT /note= "His-26"
 FT Active-site 54
 FT /note= "His-30"
 FT Active-site 58
 FT /note= "Tyr-58"
 FT Active-site 98
 FT /note= "Tyr-74"
 FT Misc-difference 155
 FT /label= Gln, Glu
 FT Active-site 167
 FT /note= "Gln-143"
 FT Active-site 183
 FT /note= "Asp-159"
 FT Active-site 185

FT Active-site /note= "Trp-161"
 FT 187
 FT /note= "His-163"
 XX
 XX WO9913088-A1.
 XX 18-MAR-1999.
 XX
 XX 10-SEP-1998; 98WO-US018842.
 XX
 XX 10-SEP-1997; 97US-00927230.
 XX
 XX (UYFL) UNIV FLORIDA.
 XX
 XX Nick HS, Silverman DN;
 XX
 XX WPI; 1999-229242/19.
 XX
 XX New recombinant human manganese superoxide dismutase proteins.
 XX
 XX Claim 2; Page 53-54; 61pp; English.
 XX
 XX This protein is human manganese superoxide dismutase (hMnSOD). Novel hMnSOD proteins having catalytic activity which differs from this natural hMnSOD are claimed (see AAW98171-77). The modified proteins exhibit reduced or no product inhibition, or have greater activity, or both, compared to natural hMnSOD. The modifications involve one or amino acid substitutions within the active site of the enzyme, especially at residues His-26, His-30, Tyr-34, His-74, Gln-143, Asp-159, Trp-161 and His-163. The modified hMnSOD, or expression vectors in which modified hMnSOD nucleic acid is linked to a promoter (preferably mammalian), can be used to protect a cell line from damage caused by superoxide radicals (claimed). They can also be used to treat subjects suffering from, or at risk of, cytotoxicity caused by superoxide radicals (claimed). As such, they can be used as antioxidants in the treatment of a variety of disorders, including inflammation (claimed), reperfusion injury following ischemia (claimed), and cellular damage caused by chemotherapeutic agents

Sequence 222 AA;
 Query Match 54.0%; Score 623; DB 2; Length 222;
 Best Local Similarity 53.6%; Pred. No. 1.5e-58;
 Matches 118; Conservative 31; Mismatches 61; Indels 10; Gaps 4;
 QY 6 SLSSVSRTFFVAPAAFI--RAKHTLPYAYDALEPSISKEIMTLHHTKHQT 63
 Db 5 AVCGTSRQ--LAPALYGLSGRQKHSPLDLYDGALEPHINAQIMQLHSHKHAAYVNNL 62
 QY 64 NAAEESYSAAGVKEDVLTQVLSALKFNGGGHINHSFWKNLAPYGSSEATLSEGPLKK 123
 Db 63 NVTEEKYQELAKGDVTAQIALQPALKFNNGGGHINHSIFWNLSPNGGGE---PKGELLE 119
 QY 124 ATEESFGSFEAFKPKFNADTAAGVSGGWMGLNPLTKKLEVTNTANODPL---LTHPI 180
 Db 120 AIKRDGSGDFKFKELTAAASVGVQSGGWMGLFNKXRAHLQIAACPNQDPLQGTGLIPL 179
 QY 181 IGVDIWEHAFYLYQKNVKPDYLAAVWSVINYKEAEARLOA 220
 Db 180 LGIDVWEHAYLYQKNVRPDYLYKAIWNVINWENVTERYMA 219

RESULT 5
 AAW98204
 ID AAW98204 standard; protein; 222 AA.
 XX
 XX AAW98204;
 XX
 XX 04-DEC-2000 (first entry)
 XX
 XX Amino acid sequence of a human manganese superoxide dismutase.
 DE Human; manganese superoxide dismutase; hMn SOD; superoxide radical;
 KW superoxide radical damage; cytotoxicity; inflammation; ischemia;

AC AAR90713;
 XX 25-MAR-2003 (revised)
 DT 06-APR-1996 (first entry)
 XX Human manganese superoxide-dismutase.
 XX Human; manganese superoxide-dismutase; T-lymphocyte; probe: cDNA;
 KW Escherichia coli; plasmid pMS8-4; N-terminal truncation; cloning;
 KW aminopeptidase; antiinflammatory; oxygen free radical scavenger;
 KW synovial inflammation; arthritis; lung fibrosis.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..24 "Pre-peptide"
 FT /note= "39..48"
 FT Region /note= "Region used to construct probe AAT15591"
 FT Misc-difference 66
 FT /note= "Gln in previously published sequence"
 FT Misc-difference 112
 FT /note= "Gln in previously published sequence"
 FT Misc-difference 132
 FT /note= "Gln in previously published sequence"
 FT Misc-difference 147..148
 FT /note= "Residues not present in previously published sequence"
 FT Region 203..213
 FT /note= "Region used to construct probe AAT15592"
 XX EP691401-A1.
 XX 10-JAN-1996.
 XX 25-MAR-1988; 95EP-00106995.
 XX 27-MAR-1987; 87US-00032734.
 PR 26-FEB-1988; 88US-00161117.
 XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
 XX Hartman JR, Beck Y, Nimrod A;
 XX WPI: 1996-059735/07.
 DR N-PSDB; AAT15589.
 XX New human manganese superoxide dismutase analogues - having a Lys and
 PT opt. His residue absent from the N-terminus, useful for treating e.g.
 PT synovial inflammation, arthritis or lung fibrosis.
 XX Example 1; Fig 1; 45pp; English.
 XX The sequence represents a human manganese superoxide-dismutase (MnSOD),
 CC and is encoded by a human T-lymphocyte cDNA isolated from a library in
 CC phage lambda-gt10 in Escherichia coli, by screening with a 5'-probe
 CC (AAT15591) and a 3'-probe (AAT15592), followed by subcloning in plasmid
 CC pBR322 to give plasmid pMS8-4. The cDNA may be expressed in e.g. E. coli
 CC for production of recombinant MnSOD. The MnSOD product may be cleaved
 CC with Aeromonas proteolytica aminopeptidase to produce an N-terminally
 CC truncated analogue with lysine and optionally histidine residues removed.
 CC The MnSOD analogue may be used in therapy of conditions associated with
 CC generation of oxygen free radicals, particularly synovial inflammation,
 CC arthritis and lung fibrosis (claimed). (Updated on 25-MAR-2003 to correct
 CC PF field.)
 XX Sequence 222 AA;
 SQ Query Match 53.9%; Score 621; DB 2; Length 222;
 Best Local Similarity 53.8%; Pred. No. 2.5e-38;
 Matches 118; Conservative 31; Mismatches 61; Indels 10; Gaps 4;
 QY 6 SLSSVSRSQTVPAAAFQ1--RAKHHTLPDPYDALEPSISKIMTLHHTKHQTYVNGL 63

Db 5 AVCGTSRQ--LAPALGVLSGRQKHSLPDLPDYGALEPHINAQIMQLHSHKHAAYNNL 62
 QY 64 NAAEESYSAAVGKEDVLTQVKLOSALKFNGGGHINSHLFWKNLAPYSGEATLSEGLPKK 123
 Db 63 NVTEERYQAEALAKGDVTAQIALQPALKFNGGGHINSHLFWKNLSPNGGGE---PKGELLE 119
 QY 124 AIEESFGSFEAFKKFNADTAAVGGSGWGLGNPLTKKLEVTTTANODPL---LTHIPI 180
 Db 120 AIKRDGSEDFKREKUTAAVGGSGWGLGNKORGLQIAACPNQDPLQGTGTLPL 179
 QY 181 IGVDIWEHAFYLYQKNVKPDYLAAMVMSVINYKEAEARLQA 220
 Db 180 LGIDVWEHAYLYQKNVRPDYLAAMVINWENVTERYMA 219
 RESULT 8
 AAW00018
 ID AAW00018 standard; protein; 222 AA.
 XX
 AC AAW00018;
 XX 25-MAR-2003 (revised)
 DT 24-OCT-1996 (first entry)
 XX Human manganese superoxide dismutase.
 DE Human manganese superoxide dismutase.
 XX Manganese superoxide dismutase; MnSOD; reperfusion injury; ischaemia;
 KW bronchial pulmonary dysplasia; inflammation; antiinflammatory.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..24
 FT /label= Sig_peptide
 FT Protein 25..222
 FT /label= Mat_protein
 XX US5540911-A.
 XX 30-JUL-1996.
 XX 09-JAN-1995; 95US-00370461.
 XX 22-NOV-1985; 85US-00801090.
 PR 12-SEP-1986; 86US-00907051.
 PR 29-OCT-1986; 86IE-00002851.
 PR 27-MAR-1987; 87US-00032734.
 PR 13-DEC-1989; 89US-00453057.
 PR 10-JUL-1992; 92US-00912213.
 PR 14-SEP-1993; 93US-00120951.
 XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
 XX Hartman JR, Beck Y;
 XX WPI: 1996-361912/36.
 DR N-PSDB; AAT34277.
 XX Use of recombinant human manganese superoxide dismutase - for treating
 PT inflammation or bronchial pulmonary dysplasia, reducing reperfusion
 PT injury or prolonging organ survival.
 XX Claim 1; Fig 1A-1C; 27pp; English.
 XX Human manganese superoxide dismutase (MnSOD) (AAW00018) catalyses the
 CC reduction of superoxide radicals to H2O2 and O2. Recombinant MnSOD can be
 CC obtd. using transformed host cells, esp. Escherichia coli cells contg. a
 CC plasmid carrying e.g. a cDNA clone (AAT34277) obtd. from a human T-cell
 CC library. The MnSOD is useful for reducing reperfusion injury, treating
 CC inflammation or bronchial pulmonary dysplasia and for prolonging survival
 CC of excised organs. (Updated on 25-MAR-2003 to correct PF field.) (Updated
 CC on 25-MAR-2003 to correct PR field.)

```

XX SQ Sequence 222 AA;
Query Match 53.9%; Score 621; DB 2; Length 222;
Best Local Similarity 53.6%; Pred. No. 2.5e-58;
Matches 118; Conservative 31; Mismatches 61; Indels 10; Gaps 4;

QY 6 SLSSVSRQTFVAPAAFOI--RAKHTLPVPYDALEPSISKEIMTLHTKHQTYVNGL 63
DB 5 AVCGTSRQ--LAPALGYLGRQKHSPLDPDYGALEPHINAQIMQLHSHKHAAYVNNL 62
QY 64 NAAEESYSAAVGKEDVLTQVKLSALKFNGGHHNHSIFWKNLAPYGSSEATLSEGPLKK 123
DB 63 NVTEEKYQALAKGDVTAQIALQPAKFNKGHHNHSIFWNLSPNGGGE---PKGELLE 119
QY 124 AIEBSFGSFEAFKKFNADTAAVQSGGWLGLNPLTKKLEVTITANODPL--LTHIPI 180
DB 120 AIKRDFGSFDFKFKELTAASVGVQSGGWLGFNKGQRGHLOIAACPNDPLQGTGLIPL 179
QY 181 IGVDIWEHAFYLYQKNVPDYLAADVSVINKEAEARLQA 220
DB 180 LGIDWEHAYLYQKNVPRDYKAIWNVINWENVTERYMA 219

RESULT 9
AAW98169 standard; protein; 222 AA.
AC AAW98169;
XX
DT 05-JUL-1999 (first entry)
DE Human native manganese superoxide dismutase.
XX
KW Superoxide dismutase; MnSOD; SOD; human; protein engineering;
KW enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
KW inflammation; reperfusion injury; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..24 "signal peptide"
FT Protein 25..222
FT Active-site 50
FT Active-site 54
FT Active-site 58
FT Active-site 98
FT Active-site 167
FT Active-site 183
FT Active-site 185
FT Active-site 187
FT Active-site 187
FT W09913088-A1.
XX
PD 18-MAR-1999.
XX
PF 10-SEP-1998; 98WO-US018842.
XX
PR 10-SEP-1997; 97US-00927230.
XX
PA (UYFL ) UNIV FLORIDA.
XX
PI Nick HS, Silverman DN;

```

```

XX WPI; 1999-229242/19.
DR N-PSDB; AAX24998.
XX
FT New recombinant human manganese superoxide dismutase proteins.
XX
FS Disclosure; Page 52-53; 61pp; English.
XX
CC This protein is human manganese superoxide dismutase (hMnSOD). Novel
CC hMnSOD proteins having catalytic activity which differs from this natural
CC hMnSOD are claimed (see AAW98171-77). The modified proteins exhibit
CC reduced or no product inhibition, or have greater activity, or both,
CC compared to natural hMnSOD. The modifications involve one or amino acid
CC substitutions within the active site of the enzyme, especially at
CC residues His-26, His-30, Tyr-34, His-74, Gln-143, Asp-159, Trp-161 and
CC His-163. The modified hMnSOD, or expression vectors in which modified
CC hMnSOD nucleic acid is linked to a promoter (preferably mammalian), can
CC be used to protect a cell line from damage caused by superoxide radicals
CC (claimed). They can also be used to treat subjects suffering from, or at
CC risk of, cytotoxicity caused by superoxide radicals (claimed). As such,
CC they can be used as antioxidants in the treatment of a variety of
CC disorders, including inflammation (claimed), reperfusion injury following
CC ischemia (claimed), and cellular damage caused by chemotherapeutic agents
CC
XX Sequence 222 AA;
Query Match 53.9%; Score 621; DB 2; Length 222;
Best Local Similarity 53.6%; Pred. No. 2.5e-58;
Matches 118; Conservative 31; Mismatches 61; Indels 10; Gaps 4;

QY 6 SLSSVSRQTFVAPAAFOI--RAKHTLPVPYDALEPSISKEIMTLHTKHQTYVNGL 63
DB 5 AVCGTSRQ--LAPALGYLGRQKHSPLDPDYGALEPHINAQIMQLHSHKHAAYVNNL 62
QY 64 NAAEESYSAAVGKEDVLTQVKLSALKFNGGHHNHSIFWKNLAPYGSSEATLSEGPLKK 123
DB 63 NVTEEKYQALAKGDVTAQIALQPAKFNKGHHNHSIFWNLSPNGGGE---PKGELLE 119
QY 124 AIEBSFGSFEAFKKFNADTAAVQSGGWLGLNPLTKKLEVTITANODPL--LTHIPI 180
DB 120 AIKRDFGSFDFKFKELTAASVGVQSGGWLGFNKGQRGHLOIAACPNDPLQGTGLIPL 179
QY 181 IGVDIWEHAFYLYQKNVPDYLAADVSVINKEAEARLQA 220
DB 180 LGIDWEHAYLYQKNVPRDYKAIWNVINWENVTERYMA 219

RESULT 10
AAW98175
ID AAW98175 standard; protein; 222 AA.
XX
XX AC AAW98175;
XX
DT 05-JUL-1999 (first entry)
DE Human manganese superoxide dismutase Q143E mutant.
XX
KW Superoxide dismutase; MnSOD; SOD; human; protein engineering;
KW enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
KW inflammation; reperfusion injury; therapy; mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..24 "signal peptide"
FT Protein 25..222
FT Active-site 50
FT Active-site 54
FT Active-site 54
FT Active-site 54

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Db 180 LGIDVWEHAYLYQKNVRPDLKAIWNVINWNTERYMA 219

RESULT 14

AAW98171

ID AAW98171 standard; protein; 222 AA.

XX AC AAW98171;

XX 05-JUL-1999 (first entry)

XX Human manganese superoxide dismutase Q143N mutant.

XX Superoxide dismutase; MnSOD; SOD; human; protein engineering;

KW enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;

KW inflammation; reperfusion injury; therapy; mutant.

XX Homo sapiens.

OS Synthetic.

XX Key

PH Location/Qualifiers

FT 1..24 "signal peptide"

FT Protein

FT 25..222

FT /note= "mature protein"

FT 50

FT /note= "His-26"

FT Active-site

FT 54

FT /note= "His-30"

FT Active-site

FT 58

FT /note= "Tyr-58"

FT Active-site

FT 98

FT /note= "Tyr-74"

FT Active-site

FT 155

FT Misc-difference

FT /label= Gln, Glu

FT 167

FT Misc-difference

FT /note= "Gln replaces Asn in wild-type hMnSOD"

FT 167

FT Active-site

FT 183

FT /note= "Gln-143"

FT Active-site

FT 185

FT /note= "Asp-159"

FT Active-site

FT 187

FT /note= "Trp-161"

FT Active-site

FT 187

FT /note= "His-163"

FT Active-site

XX WO9913088-A1.

XX 18-MAR-1999.

XX 10-SEP-1998; 98WO-US018842.

XX 10-SEP-1997; 97US-00927230.

XX (UYFL) UNIV FLORIDA.

XX Nick HS, Silverman DN;

PI WPI; 1999-229242/19.

DR New recombinant human manganese superoxide dismutase proteins.

XX Claim 15; Page 54-55; 61pp; English.

XX This protein is a Q143N mutant of human manganese superoxide dismutase (hMnSOD, see also AAW98170). Novel modified hMnSOD proteins having catalytic activity which differs from natural hMnSOD are claimed. The modified proteins (see also AAW98172-77) exhibit reduced or no product inhibition, or have greater activity, or both, compared to natural hMnSOD. The modifications involve one or amino acid substitutions within the active site of the enzyme, especially at residues His-26, His-30, Tyr-34, His-74, Gln-143, Asp-159, Trp-161 and His-163. Gln-143 and His-30 are located near the active site metal, are highly conserved, and

are involved in a hydrogen bond relay which links the active site metal-bound hydroxyl group to ordered solvent, and are thus all potentially involved in catalytic activity, product inhibition and/or enzyme stability. The particularly preferred Q143N mutant has a kcat of 0.3 m/sec and a kcat/km of 0.82/uM.sec compared to respective values of 40 m/sec and 800/uM.sec for wild-type hMnSOD. It exhibits no product inhibition. Modified hMnSODs, or expression vectors in which a modified hMnSOD nucleic acid is linked to a promoter (preferably mammalian), are used to protect a cell line from damage caused by superoxide radicals (claimed). They can also be used to treat subjects suffering from, or at risk of, cytotoxicity caused by superoxide radicals (claimed). As such, they can be used as antioxidants in the treatment of a variety of disorders, including inflammation (claimed), reperfusion injury following ischemia (claimed), and cellular damage caused by chemotherapeutic agents (claimed).

XX Sequence 222 AA;

Query Match 53.6%; Score 618; DB 2; Length 222;

Best Local Similarity 53.2%; Pred. No. 5.3e-58;

Matches 117; Conservative 31; Mismatches 62; Indels 10; Gaps 4;

Qy 6 SLSSVSRTQTEVAPAFQI--RAKHTLPDPYADALEPSISKEIMTLHTKHHTYVNGL 63

Db 5 AVCGTSRQ--LAPALGYLGRQKHSPLDLPDYGALEPHINAQIMQLHSHKHAAYVNNL 62

Qy 64 NAAEESYRAAGVKEDVLTQVKLQSKALKFNGGGHINHSLEFWKNLAPYGEATLSEGLPKK 123

Db 63 NVTREYQEAALARGDVTAQIALQFALPKFNGGGHINHSIFWTNLSFNGGGE---PKGELLE 119

Qy 124 AIBESFGSFEAFKKFNADTAAGVQSGWGWLGNPLTKLEVTITANQDPL---LTHIPI 180

Db 120 AIKRDGSGFDKFKELTAASVGQSGWGWLGNPKYKRAHLQIAACPNNDPLOGTTGLIPL 179

Qy 181 IGVDIWEHAFYLYQKNVRPDLKAIWNVINWNTERYMA 219

Db 180 LGIDVWEHAYLYQKNVRPDLKAIWNVINWNTERYMA 219

RESULT 15

AAW98174

ID AAW98174 standard; protein; 222 AA.

XX AC AAW98174;

XX 05-JUL-1999 (first entry)

XX Human manganese superoxide dismutase Q143D mutant.

XX Superoxide dismutase; MnSOD; SOD; human; protein engineering;

KW enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;

KW inflammation; reperfusion injury; therapy; mutant.

XX Homo sapiens.

OS Synthetic.

XX Key

PH Location/Qualifiers

FT 1..24

FT /note= "signal peptide"

FT Protein

FT 25..222

FT /note= "mature protein"

FT 50

FT /note= "His-26"

FT Active-site

FT 54

FT /note= "His-30"

FT Active-site

FT 58

FT /note= "Tyr-58"

FT Active-site

FT 98

FT /note= "Tyr-74"

FT Misc-difference

FT 155

FT /label= Gln, Glu

FT 167

FT Misc-difference

FT /note= "Gln replaces Asp in wild-type hMnSOD"

FT 167

FT Active-site

Job time : 63 secs

FT Active-site /note= "Gln-143"
FT 183
FT Active-site /note= "Asp-159"
FT 185
FT Active-site /note= "Trp-161"
FT 187
FT /note= "His-163"

XX WO9913088-A1.

XX 18-MAR-1999.

XX 10-SEP-1998; 98WO-US018842.

XX 10-SEP-1997; 97US-00927230.

XX (UYFL) UNIV FLORIDA.

XX Nick HS, Silverman DN;

XX WPI; 1999-229242/19.

XX New recombinant human manganese superoxide dismutase proteins.

XX Claim 14; Page; 61pp; English.

XX This protein is a Q143D mutant of human manganese superoxide dismutase (hMnSOD, see also AA98170). Novel modified hMnSOD proteins having catalytic activity which differs from natural hMnSOD are claimed. The modified proteins (see also AA98171-77) exhibit reduced or no product inhibition, or have greater activity, or both, compared to natural hMnSOD. The modifications involve one or amino acid substitutions within the active site of the enzyme, especially at residues His-26, His-30, Tyr-34, His-74, Gln-143, Asp-159, Trp-161 and His-163. Gln-143, Tyr-34 and His-30 are located near the active site metal, are highly conserved, and are involved in a hydrogen bond relay which links the active site metal-bound hydroxyl group to ordered solvent, and are thus all potentially involved in catalytic activity, product inhibition and/or enzyme stability. Modified hMnSODs, or expression vectors in which a modified hMnSOD nucleic acid is linked to a promoter (preferably mammalian), are used to protect a cell line from damage caused by superoxide radicals (claimed). They can also be used to treat subjects suffering from, or at risk of, cytotoxicity caused by superoxide radicals (claimed). As such, they can be used as antioxidants in the treatment of a variety of disorders, including inflammation (claimed), reperfusion injury following ischemia (claimed), and cellular damage caused by chemotherapeutic agents. Note. The present sequence is not shown in the specification but is derived from the hMnSOD sequence given on page 53-54

XX Sequence 222 AA;

Query Match 53.6%; Score 618; DB 2; Length 222;

Best Local Similarity 53.2%; Pred. No. 5.3e-58;

Matches 117; Conservative 31; Mismatches 62; Indels 10; Gaps 4;

QY 6 SLSSVSROTFVAPAFQI--RAKHTLPPLPYADALEPSISKEIMTLHTKHQTVVNGL 63

Db 5 AVCCTSRQ--LAPALGILGSRQKHSPLDLPYDGALEPHINAIQIMQHSKHAAVYNNL 62

QY 64 NAAEESYSAAGKEDVLTQVKLSALKFNGGGHINHSFLWKNLAPYGSEATLSEGLKK 123

Db 63 NVTEEKYQALAKGDVDTAQIALQPALKFGGGHINHSIFWTNLSPNGGGE---PKGELLE 119

QY 124 AIEESFGSEAPKKFNADTAAGSGGCMGLGNPLTKKLEVTITANQDPL---LTHIFI 180

Db 120 AIKRDGSGDFKFKELTAASVGVGGGCMGLGNPKKXRAHLQIAACPNDPLOTGTLIPL 179

QY 181 IGVDIWEHAFYLYQKNVDPDYLAAVMSVINYKEAEARLOA 220

Db 180 LGIDWEHAYLYQKNVREDYLYKAIWNVINWENVTERYNA 219

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2004, 17:09:18 ; Search time 22 seconds
(without alignments)
520.953 Million cell updates/sec

Title: US-09-727-855B-5

Perfect score: 1153

Sequence: 1 MSVRASLSVSRTQTFVAPAA.....AAVWSVNTKEARLQAAL 222

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	692	60.0	224	4	US-09-091-097-8
2	668.5	58.0	206	4	Sequence 8, Appli
3	623	54.0	222	2	Sequence 6, Appli
4	623	54.0	222	2	Sequence 2, Appli
5	618	53.6	222	3	US-08-927-230A-2
6	618	53.6	222	2	US-09-151-052-2
7	618	53.6	222	2	US-08-365-486A-28
8	618	53.6	222	2	Sequence 28, Appl
9	617	53.5	222	3	Sequence 3, Appli
10	617	53.5	222	3	Sequence 28, Appl
11	617	53.5	222	2	Sequence 44, Appl
12	610	52.9	198	6	Sequence 52, Appl
13	607	52.6	198	3	Sequence 2, Appli
14	607	52.6	226	3	Sequence 44, Appl
15	606	52.6	198	6	Patent No. 5240847
16	570	49.4	230	2	Sequence 30, Appl
17	570	49.4	230	2	US-08-928-692-30
18	536	46.5	177	6	Sequence 30, Appl
19	513.5	44.5	214	4	US-09-198-452A-75
20	498.5	43.2	217	4	US-09-489-039A-12227
21	496	43.0	204	1	US-08-445-909A-29
22	495	42.9	204	1	US-08-445-909A-17
23	482.5	41.8	196	4	US-08-679-493A-185
24	479	41.5	200	4	Sequence 185, App
25	478.5	41.5	224	4	Sequence 2, Appli
26	465.5	40.4	201	4	US-09-543-681A-6654
27	462	40.1	233	2	Sequence 3584, Ap
					Sequence 31, Appl

28 462 40.1 233 4 US-09-339-972-31
29 461 40.0 207 4 US-09-252-991A-24593
30 454.5 39.4 241 4 US-09-540-236-3442
31 444.5 38.6 207 4 US-09-214-909-24
32 430.5 37.3 188 4 US-09-262-856A-6
33 367 31.8 219 4 US-09-328-352-4346
34 358.5 31.1 205 4 US-09-543-681A-4456
35 349.5 30.3 227 4 US-09-489-039A-9633
36 337.5 29.3 245 4 US-09-252-991A-24333
37 326 28.3 214 3 US-09-411-578-1
38 326 28.3 214 4 US-09-749-233-1
39 312 27.1 190 4 US-08-679-493A-184
40 201.5 17.5 213 3 US-09-008-303-2
41 104 9.0 30 4 US-09-091-097-52
42 103.5 9.0 835 4 US-09-458-457-8
43 103.5 9.0 835 4 US-09-947-199A-8
44 93.5 8.1 2016 4 US-09-475-252-2
45 89.5 7.8 373 3 US-09-039-198A-14

ALIGNMENTS

RESULT 1
US-09-091-097-8
; Sequence 8, Application US/09091097
; Patent No. 6432407
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH
; APPLICANT: OKADO, TAKASHI
; APPLICANT: YAGIHARA, TOMOKO
; APPLICANT: KURODA, MASANOBU
; APPLICANT: ONISHI, YOSHIMI
; APPLICANT: KATO, IKUNOSHIN
; APPLICANT: AKIYAMA, KAZUO
; APPLICANT: YASUEDA, HIROSHI
; APPLICANT: YAMAGUCHI, HIDEYO
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
; TITLE OF INVENTION: MALASSEZIA
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/091,097
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0346P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 224 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-091-097-8
Query Match 60.0%; Score 692; DB 4; Length 224;
Best Local Similarity 59.3%; Pred. No. 4.8e-73;


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124 AIESFGSGFEAKKKFNADTAAVQSGSGWGLGNPLTKKLEVTTTANQDPL---LTHDPI 180
Qy
120 AAKKGGGDFKFKELKLTAAASVQSGSGWGLGNPKKXRAHLLTAACFNQDPLQGTGLTLP 179
Db
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RESULT 4
US-09-151-052-2
; Sequence 2, Application US/09151052
; Patent No. 6107070
; GENERAL INFORMATION:
; APPLICANT: Nick et al.
; TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD
; STREET: 28 State Street, Floor 24
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/151.052

```

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1 CLASSIFICATION:
2
3 PRIOR APPLICATION DATA:
4   APPLICATION NUMBER: 08/927,230
5   FILING DATE: September 10, 1997
6   ATTORNEY/AGENT INFORMATION:
7     NAME: Remillard, Jane
8     REGISTRATION NUMBER: 38,872
9     REFERENCE/DOCKET NUMBER: UPJ-001
10    TELECOMMUNICATION INFORMATION:
11      TELEPHONE: (617)227-7400
12      TELEFAX: (617)742-4214
13
14    INFORMATION FOR SEQ ID NO: 2:
15      SEQUENCE CHARACTERISTICS:
16        LENGTH: 222 amino acids
17        TYPE: amino acid
18        TOPOLOGY: linear
19      MOLECULE TYPE: protein
20      FEATURE:
21        NAME/KEY: OTHER
22        LOCATION: 131
23      OTHER INFORMATION: Xaa can code for Gln or Glu
24
25 US-09-151-052-2

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Query Match	54.0%	Score 623;	DB 3;	Length 222;
Best Local Similarity	53.6%;	Pred. No. 6.2e-65;		
Matches 118;	Conservative 31;	Mismatches 61;	Indels 10;	Gaps 4;
QY	6	SLSSVSQTTVPAAFOI--RAKHTLPYDALEPSISKETMTLHHTKHQHTYVNGL	63	
Db	5	AVGCTSRQ--LAPALGYLGRQKHSLPDLPYDYGALPEHINAQIMQGLHSHKHAAYVNNL	62	
QY	64	NAAEESYSAAGKEDVLITOVKIQALAKFNGGGHINHSLFWKNLAPYSGSEATLSEGLPKK	123	
Db	63	NVTEEKQEALAKGDVTAQIALQPALKFNFGGGHINHSLFWNLSPNGGGE---PQGELE	119	
QY	124	AIBESFGSFAPKKFNADTAAGVSGSGWGLGNPLTKLEVTTTANQDPL---LTHIPI	180	
Db	120	AIRKDFSGDFKFEKLTAASVGVSGSGWGLGFNKRRAHLQIAACPNQDPLQGTGTGLPL	179	
QY	181	IGVDIWEHAPYLOQYKNYKPDYLAAVWSVINYKEAEARLQA	220	

DB 180 LGIDVWEHAYLYQKNVPRDYLKAIWNVINWENTERYMA 2119

RESULT 5
US-08-365-486A-28
; Sequence 28, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-365-486A-28

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Query Match 53.6%; Score 618; DB 2; Length 222;
Best Local Similarity 53.6%; Pred. No. 2.4e-64;
Matches 118; Conservative 31; Mismatches 61; Indels

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Db	5	AVCGTSG--LAPALGVLSGRKSHLDPLPYDYGALPEPHINAQIMQLHSHKHAAAYVNNL	62
QY	64	NAABESYSAAVGKEDVLTQVYLOSALKFNGGGHINSHLPWKNLAPVGSSEATLSSEGPLKK	123
Db	63	NWNEKYQEAUKGDVTAQALOPALKFNGGGHINSHIFWNLSPNGGGE---PKGELLE	119
QY	124	ATIESFGFEAFKKFNADTAAVQSGSGWGLGNPLTKLEVTVTANQPL--LTHIPI	180
Db	120	AIKRDFGSFDFKEKLTAAVGVGVSGSGWGLFNKRGHLOIAACFNQDPLQGTGLDLP	179
QY	181	IGVDIWEHAFYLOKYNKVPDYLAAMVSVINYKEAEARLQA	220
Db	180	LGIDIDWEHAYFYLOKYNRPDYLAAMVSVINWENVTERYMA	219

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RESULT 6
US-08-927-230A-3
; Sequence 3, Application US/08927230A
; Patent No. 5985633
; GENERAL INFORMATION:
; APPLICANT: Nick et al.
; TITLE OF INVENTION: Human Mangano
; NUMBER OF SEQUENCES: 11

```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street, Floor 24
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
;
; ZIP: 02109-1875
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,230A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 435
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: UFJ-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 131
; OTHER INFORMATION: Xaa can code for Gln or Glu
;
; US-08-927-230A-3
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; Query Match 53.6%; Score 618; DB 2; Length 222;
; Best Local Similarity 53.2%; Pred. No. 2.4e-64;
; Matches 117; Conservative 31; Mismatches 62; Indels 10; Gaps 4;
;
; QY 6 SLSSVSRTFTVAPAAFI--RAKHTLPPLPAYDALEPSISKEIMTLHHTKHQTYVNGL 63
; DB 5 AVCGTSRQ--LAPALGYLSGRQKHSPLDIPYDGALEPHINAQIMQLHSHKHAAYVNNL 62
; QY 64 NAAESYSAAVGKEDVLTQVKLSALKFNGGGHINHSIPWKNLAPYGSSEATLSGGLKK 123
; DB 63 NVTEEKYQBALAKGDVTAQIALQPAKFKNGGGHINHSIPWNLSPNGGGE---PKGELLE 119
; QY 124 AIEESFGSFEAPKKFNADTAAVQSGWGLGNPLTKKLEVTITANODPL---LTHIPI 180
; DB 120 AIKRDGFSDFKFKELTAASVQSGWGLGNFKXKRAHLQIAACPNNDPLQGTGLIPL 179
; QY 181 IGVDTWEHAFYLYQKNVPDYLAAVMSVINYKEAEARLQA 220
; DB 180 LGIDVWEHAYLYQKNVPDYLKAIWNVINWENVTERYMA 219
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; RESULT 7
; US-09-151-052-3
; Sequence 3, Application US/09151052
; Patent No. 6107070
; GENERAL INFORMATION:
; APPLICANT: Nick et al.
; TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Floor 24
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street, Floor 24
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
;
; ZIP: 02109-1875
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,230A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 435
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: UFJ-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 131
; OTHER INFORMATION: Xaa can code for Gln or Glu
;
; US-09-151-052-3
;
; Query Match 53.6%; Score 618; DB 2; Length 222;
; Best Local Similarity 53.2%; Pred. No. 2.4e-64;
; Matches 117; Conservative 31; Mismatches 62; Indels 10; Gaps 4;
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; QY 6 SLSSVSRTFTVAPAAFI--RAKHTLPPLPAYDALEPSISKEIMTLHHTKHQTYVNGL 63
; DB 5 AVCGTSRQ--LAPALGYLSGRQKHSPLDIPYDGALEPHINAQIMQLHSHKHAAYVNNL 62
; QY 64 NAAESYSAAVGKEDVLTQVKLSALKFNGGGHINHSIPWKNLAPYGSSEATLSGGLKK 123
; DB 63 NVTEEKYQBALAKGDVTAQIALQPAKFKNGGGHINHSIPWNLSPNGGGE---PKGELLE 119
; QY 124 AIEESFGSFEAPKKFNADTAAVQSGWGLGNPLTKKLEVTITANODPL---LTHIPI 180
; DB 120 AIKRDGFSDFKFKELTAASVQSGWGLGNFKXKRAHLQIAACPNNDPLQGTGLIPL 179
; QY 181 IGVDTWEHAFYLYQKNVPDYLAAVMSVINYKEAEARLQA 220
; DB 180 LGIDVWEHAYLYQKNVPDYLKAIWNVINWENVTERYMA 219
;
; RESULT 8
; US-08-880-342-28
; Sequence 28, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Manette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-880-342-28

Query Match 53.6%; Score 618; DB 3; Length 222;
Best Local Similarity 53.6%; Pred. No. 2.4e-64;

Matches 118; Conservative 31; Mismatches 61; Indels 10; Gaps 4;

QY 6 SLSSVSQRTFVAPAAFI--RAKHTLPELPYADALEPSISKETMTLHHTKHHTQYVNGL 63
Db 5 AVCGTSRQ--LAPALGYLGRQRKHSUPDLDYDYGALPEHINAQIMQLHSHKHAAYVNNL 62
QY 64 NAAEESYSAAGKEDVLTVQKLSALKFNGGGHINSLFWKNLAPYSGSEATLSEGLPKK 123
Db 63 NVNEEKYQELAKGDVTAQIALQALPKFNGGGHINHSIFWTNLSPNGGGE---PKGELLE 119
QY 124 AIEESFGSPFAFKKFNADTAAGVGGSGWGLNPLTKLEVTITANQDPL---LTHIPI 180
Db 120 AIKRDFSGDFKFKELTAASVGVGGSGWGLGFKNGKRGHILQIAACPNQDPLQGTGTGLIPL 179
QY 181 IGVDIWEHAFYLOKKNKPDYLAAVSVNYNKEAEARLQA 220
Db 180 LGIDVWEHAYLYQKNRDPYDKAIWNVINWENTERYMA 219

RESULT 9

US-08-023-980B-44
Sequence 44, Application US/08023980B
Patent No. 5843641
GENERAL INFORMATION:
APPLICANT: Brown, Robert
APPLICANT: Horvitz, H. Robert
APPLICANT: Rosen, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
PREVENTION AND TREATMENT OF DISEASES OF CELL DEATH
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 585 Commercial Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-1024
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/023,980B
FILING DATE: 26-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/177001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/723-4123
TELEFAX: 617/723-8962
TELEX:
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-023-980B-44

Query Match 53.5%; Score 617; DB 2; Length 222;
Best Local Similarity 53.6%; Pred. No. 3.2e-64;

Matches 118; Conservative 30; Mismatches 62; Indels 10; Gaps 4;

QY 6 SLSSVSQRTFVAPAAFI--RAKHTLPELPYADALEPSISKETMTLHHTKHHTQYVNGL 63
Db 5 AVCGTSRQ--LAPALGYLGRQRKHSUPDLDYDYGALPEHINAQIMQLHSHKHAAYVNNL 62
QY 64 NAAEESYSAAGKEDVLTVQKLSALKFNGGGHINSLFWKNLAPYSGSEATLSEGLPKK 123
Db 63 NVNEEKYQELAKGDVTAQIALQALPKFNGGGHINHSIFWTNLSPNGGGE---PKGELLE 119
QY 124 AIEESFGSPFAFKKFNADTAAGVGGSGWGLNPLTKLEVTITANQDPL---LTHIPI 180
Db 120 AIKRDFSGDFKFKELTAASVGVGGSGWGLGFKNGKRGHILQIAACPNQDPLQGTGTGLIPL 179
QY 181 IGVDIWEHAFYLOKKNKPDYLAAVSVNYNKEAEARLQA 220
Db 180 LGIDVWEHAYLYQKNRDPYDKAIWNVINWENTERYMA 219

RESULT 10

US-08-486-953A-52
Sequence 52, Application US/08486953A
Patent No. 5849290
GENERAL INFORMATION:
APPLICANT: Brown, Robert
APPLICANT: Horvitz, H. Robert
APPLICANT: Rosen, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
PREVENTION AND TREATMENT OF DISEASES OF CELL DEATH
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,953A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,052
FILING DATE: 28-FEB-1994
ATTORNEY/AGENT INFORMATION:

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; APPLICATION NUMBER: US Unknown
; FILING DATE: 03-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: McMillian, Nabeela R.
; REGISTRATION NUMBER: P-43,363
; REFERENCE/DOCKET NUMBER: UTSD:560
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-126-109-2

Query Match 53.5%; Score 617; DB 3; Length 222;
Best Local Similarity 53.6%; Pred. No. 3.2e-64;
Matches 118; Conservative 30; Mismatches 62; Indels 10; Gaps 4;

Qy 6 SLSSVSQTFVADAAAFQI--RAKHTLPQLPYAVYDALEPSISKEIMTLHHTKHHTYVNGL 63
Db 5 AVCGTSQ--LAPALGYLGRSQKHSLPDLPIYDGALEPHINAQIMJHSHKHAAYVNNL 62
Qy 64 NAAEESYSAAVGGEDVLTVQKLSALFKNGGGGHINHSLPWKNIAPYGESEATLSEGLKK 123
Db 63 NVTEEKYQEAIAKGDVTAQIALQPAKXFGGGGHINHSIFWNLSPNGGGE---PKGELLE 119
Qy 124 AIBESFGSFAFKKKFNADTAAGVSGGWGLGNPLTKKLEVTVTANQDDL---LTHIPI 180
Db 120 AIKEDFGSFKFEKLTAAASVGVGSGGWGLGPNKERGHILQIAACPQDPLQGTTLGL 179
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Db 180 LGIDVWEHAYLYQXNVKPDYLAIAWNVINWENVTERYMA 219

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RESULT 12
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; Patent No. 5240847
; APPLICANT: HECKL, KONRAD; SPEVAK, WALTER; OSTERMANN, ELINBORG;
; ZOPHEL, ANDREAS; KRYSTEK, EDELTRAUD; MAURER-FOGY, INGRID;
; WICHE-CASTANON, MARIA J.; SUPRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
; TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
; (HMN-SOD)
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/167,261
; FILING DATE: 11-MAR-1988
; SEQ ID NO:10:
; LENGTH: 198
5240847-10

Query Match          52.9%; Score 610; DB 6; Length 198;
Best Local Similarity 56.1%; Pred. No. 1.8e-63;
Matches 111; Conservative 27; Mismatches 54; Indels 6; Gaps 2;

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Qy      86 QSALKFNGGGHINHSFLWKNLAPYGSSEATLSEGPLKKAIBESTGSGFEAFKKKFNADTAA 145
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Qy      146 VQSGSGWGLGNPLTKKLEVTTTANQDPL---LTHPIPIGVDIWEHAFYLOYKNVKPYDL 202
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```

```

CORRESPONDENCE ADDRESS:
ADDRESS: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: CO
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,019
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2848-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 226 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-075-019-7

Query Match 52.6%; Score 607; DB 3; Length 226;
Best Local Similarity 56.1%; Pred. No. 4.9e-63;
Matches 11; Conservative 26; Mismatches 55; Indels 6; Gaps 2

QY 26 KHTLPPLPAYDALEPSISKEIMTLHTKHQTYVNGLNAAEESYSAAVGKEDVLTQVKL 85
DB 3 KHSLPDLPYDYGALPHINAQIMQLHSHKHAAYVNNLNVTTEKYQBALAKGDTVTAQTAL 62

QY 86 QSALKNGGGHHNSLFWKNLAPVGSSEATLSEGPLKKAIEESFGSPAPKKFNADTAA 145
DB 63 QPALKFNGGGHHNSIFWTNLSNPGGE---PKGELLEAIKRDFSGDFKFKELTAASVG 119

QY 146 VQSGGWGLGNPLTKKLEVTTTANQDPL--LTHPIPLIGVDIWEHAPYLOYNKVPDYL 202
DB 120 VQSGGWGLGNFNGRGLHQLTAACPNDPLOGTTGLIFLLGIDWEHAYLYQKNVRPDL 179

QY 203 AAVSVNVYKAEARLQA 220
DB 180 KATWNVINWENVTRYMA 197

RESULT 15
5240847-11
; APPLICANT: HECKL, KONRAD; SPEVAK, WALTER; OSTERMANN, ELINBORG;
; ZOPHEL, ANDREAS; KRYSSTEK, EDELTRAUD; MAURER-FOGY, INGRID;
; WICHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
; TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
; (HMN-SOD)
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/167,261
; FILING DATE: 11-MAR-1988
; SEQ ID NO: 11:
; LENGTH: 198
5240847-11

Query Match 52.6%; Score 606; DB 6; Length 198;
Best Local Similarity 55.8%; Pred. No. 5.2e-63;
Matches 110; Conservative 28; Mismatches 54; Indels 6; Gaps 2

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Qy	146	VQSGSGWGLNPLTKKLEVTTTANQDPL--LTHIPIIGVDIWEHAFYLOYKNVCPDYL	202
Db	118	VQSGSGWGLGENKERGHLQIAACPNQDPLQGTGLIPLLGIDVWEHAYLOYKNVRDYL	177
Qy	203	AAVWSVINYKEAEARLQA	220
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Job time : 23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 30, 2004, 17:09:18 ; Search time 42 Seconds
(without alignments)
1383.070 Million cell updates/sec

Title: US-09-727-855B-5

Perfect score: 1153

Sequence: 1 MSVRASLSVSRQTFVAPAA.....AAVWSVINYKEARLQAL 222

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1065169 seqs, 261661801 residues

Total number of hits satisfying chosen parameters: 1065169

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pap.*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pap.*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	741.5	64.3	198	9 US-09-727-855B-7	Sequence 7, Appli
4	692	60.0	224	14 US-10-109-670-11	Sequence 11, Appl
5	668.5	58.0	206	14 US-10-109-670-10	Sequence 10, Appl
6	634.5	55.0	222	14 US-10-230-331-22	Sequence 22, Appl
7	629.5	54.6	222	14 US-10-230-331-20	Sequence 20, Appl
8	618	53.6	222	14 US-10-230-331-19	Sequence 19, Appl
9	603.5	52.3	240	12 US-10-424-599-233245	Sequence 233245,
10	602.5	52.3	241	12 US-10-424-599-233247	Sequence 233247,
11	592	51.3	202	14 US-10-230-331-21	Sequence 21, Appl
12	589	51.1	233	15 US-10-310-154-662	Sequence 662, App
13	586	50.8	235	14 US-10-230-331-26	Sequence 26, Appl
14	582	50.5	228	14 US-10-230-331-25	Sequence 25, Appl
15	556.5	48.3	233	14 US-10-230-331-24	Sequence 24, Appl

16	513.5	44.5	214	15 US-10-289-762-75	Sequence 75, Appl
17	502	43.5	887	14 US-10-130-973A-6	Sequence 6, Appli
18	502	43.5	907	14 US-10-130-973A-5	Sequence 5, Appli
19	495	42.9	685	14 US-10-130-973A-7	Sequence 7, Appli
20	495	42.9	862	14 US-10-130-973A-4	Sequence 4, Appli
21	495	42.9	882	14 US-10-130-973A-3	Sequence 3, Appli
22	479	41.5	200	9 US-09-818-564-2	Sequence 2, Appli
23	479	41.5	200	9 US-09-738-626-6727	Sequence 6727, Ap
24	462	40.1	233	14 US-10-230-331-28	Sequence 28, Appl
25	430.5	37.3	188	9 US-09-987-190-6	Sequence 12947, A
26	414	35.9	213	14 US-10-156-761-12947	Sequence 23, Appl
27	339.5	29.4	193	14 US-10-230-331-23	Sequence 663, App
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31	327.5	28.4	218	12 US-10-335-977-7868	Sequence 59803, A
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37	258	22.4	386	12 US-10-425-114-59796	Sequence 6, Appl
38	255	22.1	95	9 US-09-993-333-12	Sequence 188362,
39	246	21.3	171	12 US-10-424-599-188362	Sequence 233242,
40	232	20.1	169	12 US-10-424-599-233242	Sequence 70586, A
41	227.5	19.7	175	12 US-10-425-114-70586	Sequence 59797, A
42	222	19.3	225	12 US-10-425-114-59797	Sequence 59795, A
43	195.5	17.0	311	12 US-10-425-114-59795	Sequence 59794, A
44	191	16.6	240	12 US-10-425-114-59794	Sequence 59362, A
45	190.5	16.5	218	12 US-10-425-114-59362	

ALIGNMENTS

RESULT 1

US-09-727-855B-5
; Sequence 5, Application US/09727855B
; Patent No. US20020168703A1
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUL
; TITLE OF INVENTION: MATERIALS THEREOF
; FILE REFERENCE: C38435/111694
; CURRENT APPLICATION NUMBER: US/09/727,855B
; FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Phaffia rhodozyma
US-09-727-855B-5

Query Match	100.0%	Score 1153	DB 9	Length 222
Best Local Similarity	100.0%	Pred. No. 4e-114		
Matches 222	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MSVRASLSVSRQTFVAPAAQIRAKHTLPELPYADALEPSISKEIMTLHHTKHQTYV	60	
Db	1	MSVRASLSVSRQTFVAPAAQIRAKHTLPELPYADALEPSISKEIMTLHHTKHQTYV	60	
QY	61	NGLNAAEESYSAVGKEDVLTQVKLSALKFNGGGHNSLFWKNLAPYGESEATLSEGP	120	
Db	61	NGLNAAEESYSAVGKEDVLTQVKLSALKFNGGGHNSLFWKNLAPYGESEATLSEGP	120	
QY	121	LKKAIBESFGSFEAFKKFNADTAQVQSGWGLGNPLTKKLEVTITANQDPLTHIPI	180	
Db	121	LKKAIBESFGSFEAFKKFNADTAQVQSGWGLGNPLTKKLEVTITANQDPLTHIPI	180	
QY	181	IGVDIWEHAFYIQKNVKPDYLAAMVSNVINYKEARLQAL	222	

Db 181 IGVDIWEHAFYQYKVNKPDYLAADVSVINKEAEARLQAL 222
 |||||
 RESULT 2
 US-10-230-331-27
 ; Sequence 27, Application US/10230331
 ; Publication No. US20030157513A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RAJASEKHARAN, Ram
 ; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
 ; FILE REFERENCE: 110522
 ; CURRENT APPLICATION NUMBER: US/10/230,331
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/315,757
 ; PRIOR FILING DATE: 2001-08-30
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 27
 ; LENGTH: 200
 ; TYPE: PRT
 ; ORGANISM: Ganoderma microsporum
 US-10-230-331-27
 Query Match 64.9%; Score 748.5; DB 14; Length 200;
 Best Local Similarity 71.6%; Pred. No. 3.6e-71;
 Matches 141; Conservative 24; Mismatches 23; Indels 9; Gaps 3;
 Qy 27 HTLPDPYDALPESISKEIMTLHHTKHQTYVNGLNAAESYS-AAVGKEDVLTQVKL 85
 |||||
 Db 3 HVLDPDPYVNALEPFISQIMELHKKHHTQTYVNSLNAAEQAVAKASTPKX-RIAL 58
 |||||
 Qy 86 QSALKFNGGGHINSLFWKNLAPYGS-EEATLSEGLKKAIEESFGSFEAPKPKKENA 141
 |||||
 Db 59 QSALKFNGGGHINSLFWKNLAPAKSEKGGKGLADGLPKSALEQNNWGSVDNFIKEFNA 118
 |||||
 Qy 142 DTAAVQSGGWLGLNPLTKKLEVTITANQDPLTHIPIIGVDIWEHAFYQYKVNKPDY 201
 |||||
 Db 119 TTAALQSGGWLGLNPLTKKLEVTITANQDPLTHIPIIGVDIWEHAFYQYKVNKADY 178
 |||||
 Qy 202 LAADVSVINKEAEARL 218
 |||||
 Db 179 LAADVSVINKEAEARL 195
 |||||
 RESULT 3
 US-09-727-855B-7
 ; Sequence 7, Application US/09727855B
 ; Patent No. US20020168703A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HOSHINO, Tatsuo
 ; APPLICANT: OJIMA, Kazuyuki
 ; APPLICANT: SETOGUCHI, Yutaka
 ; TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUL
 ; FILE REFERENCE: C38435/111694
 ; CURRENT APPLICATION NUMBER: US/09/727,855B
 ; CURRENT FILING DATE: 2000-12-01
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 198
 ; TYPE: PRT
 ; ORGANISM: Phaffia rhodozyma
 US-09-727-855B-7
 Query Match 64.3%; Score 741.5; DB 9; Length 198;
 Best Local Similarity 69.7%; Pred. No. 2e-70;
 Matches 138; Conservative 20; Mismatches 37; Indels 3; Gaps 1;
 Qy 25 AKHLPDPYDALPESISKEIMTLHHTKHQTYVNGLNAAESYSAAVGKEDVLTQVK 84
 |||||
 Db 2 APYTLDPYDALPESISKEIMTLHHTKHQTYVNGLNAAEQAFSQT-NDIKAQIA 58
 |||||

Qy 85 QSALKFNGGGHINSLFWKNLAPYGSSEATLSEGLKKAIEESFGSFEAPKPKKFNADTA 144
 |||||
 Db 59 QSALKFNGGGHINSLFWKNLAPADSAKLTGSLKTAIDKDFGSEFEKPKFNATL 118
 |||||
 Qy 145 AVQSGGWLGLNPLTKKLEVTITANQDPLTHIPIIGVDIWEHAFYQYKVNKPDYLA 204
 |||||
 Db 119 GVQSGGWLGLNTATKHLIATITANQDPLTHIPIIGVDIWEHAFYQYKVNKPDYLA 178
 |||||
 Qy 205 VMSVINKEAEARLQAL 222
 |||||
 Db 179 FMVNCFAEAQRREDAV 196
 |||||
 RESULT 4
 US-10-109-670-11
 ; Sequence 11, Application US/10109670
 ; Publication No. US20030105283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TAKESAKO, KAZUTOH et al.
 ; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA
 ; FILE REFERENCE: 1422-0523P
 ; CURRENT APPLICATION NUMBER: US/10/109,670
 ; CURRENT FILING DATE: 2002-04-01
 ; NUMBER OF SEQ ID NOS: 58
 ; SEQ ID NO 11
 ; LENGTH: 224
 ; TYPE: PRT
 ; ORGANISM: Malassezia furfur
 US-10-109-670-11
 Query Match 60.0%; Score 692; DB 14; Length 224;
 Best Local Similarity 59.3%; Pred. No. 4.4e-65;
 Matches 128; Conservative 31; Mismatches 53; Indels 4; Gaps 1;
 Qy 11 SRQTFVAP-APQTRAKHTLPYAYDALPESISKEIMTLHHTKHQTYVNGLNAA 66
 |||||
 Db 6 TRRAAAPLANAAQMGVTKYTLPLPYDYGALPEAISGEIMETHYKHHRTYVNNLAA 65
 |||||
 Qy 67 EESYSAVKGEDVLTQVKLSALKFNGGGHINSLFWKNLAPYGSSEATLSEGLKKAIE 126
 |||||
 Db 66 EDKLIDALPQOSPLGETAQLNAIFNGGGHINSLFWKNLAPTKNGGELDSGEURSAID 125
 |||||
 Qy 127 ESFGSFEAPKPKFNADTAAVQSGGWLGLNPLTKKLEVTITANQDPLTHIPIIGVDI 186
 |||||
 Db 126 RDFSVDAMKEFNALAGIQQSGGWLGLNPTTKLDIITANQDPLTHIPIIGVDI 185
 |||||
 Qy 187 EHAFYQYKVNKPDYLAADVSVINKEAEARLQAL 222
 |||||
 Db 186 EHAFYQYKVNKADYFKAITVINFEEAEKRLKEAL 221
 |||||

RESULT 5
 US-10-109-670-10
 ; Sequence 10, Application US/10109670
 ; Publication No. US20030105283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TAKESAKO, KAZUTOH et al.
 ; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA
 ; FILE REFERENCE: 1422-0523P
 ; CURRENT APPLICATION NUMBER: US/10/109,670
 ; CURRENT FILING DATE: 2002-04-01
 ; NUMBER OF SEQ ID NOS: 58
 ; SEQ ID NO 10
 ; LENGTH: 206
 ; TYPE: PRT
 ; ORGANISM: Malassezia furfur
 US-10-109-670-10
 Query Match 58.0%; Score 668.5; DB 14; Length 206;
 Best Local Similarity 63.1%; Pred. No. 1.2e-62;
 Matches 123; Conservative 24; Mismatches 47; Indels 1; Gaps 1;


```

QY 23 IRAKHTLPPLPYAYDALEPSISKEIMTLHHTKHQTQYVGNLAAEESYSAAGVKEDVLQ 82
Db 3 VMTEYTLPLPLPYAYDALEPSISKEIMTVHDKKHQTQYVGNLAAEAKAYABATAANDVLQ 62

QY 83 VKLQSALEKFGGHHNSLFWKQLAPYGSSEATLSEGPLKKAIESFGSFAPKKKNAD 142
Db 63 IQQSALEKFGGHHNSLFWKQLAPOSEGGQQLNDGPLKQAIBQBFDFEKFXTTNTK 122

QY 143 TAAVQSGGWLGLNPLTKKLEVTTTANQDPLTHPIIGVDIWEHAFYLYQKNVDPYL 202
Db 123 AAGIQSGGWLGLVAP-TGNLDLVVAKDQDPLTHHPIGVIGDGEHAWYLYQKNDKASYL 181

QY 203 AAVSVVINYKEAEAR 217
Db 182 KAWNVVNWAEAEKR 196

RESULT 6
US-10-230-331-22
; Sequence 22, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 22
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-230-331-22

Query Match
Best Local Similarity 55.0%; Score 634.5; DB 14; Length 222;
Matches 123; Conservative 30; Mismatches 58; Indels 11; Gaps 4;

QY 1 MSVRASLSVSRTQTFVAPAAQI--RAKHTLPPLPYAYDALEPSISKEIMTLHHTKHQT 58
Db 1 MLCRAACASGR---LGPAASTAGSRKHSLPDPYDYGALPHEPHINAQIMQLHHSKHAT 57

QY 59 YVGNLAAEESYSAAGVKEDVLTVKLSALKFNGGHHNSLFWKQLAPYGSSEATLSE 118
Db 58 YVNNLVNTEKYEALAKGDVTTQVALQPAKFGGHHNSLFWKQLAPYGSSEATLSE 114

QY 119 GPLKKAIESFGSFAPKKKNADTAAGVQSGGWLGLNPLTKKLEVTTTANQDPL---L 175
Db 115 GELLEAKRDFGSFEKFEKLTAVSVGVQSGGWLGLNPLTKKLEVTTTANQDPLQGT 174

QY 176 THPIIGVDIWEHAFYLYQKNVDPYLAAVSVINYKEAEAR 217
Db 175 GLIPLGIDWEHAYLYQKNVRPDLKAIWNVINWENVSQR 216

RESULT 7
US-10-230-331-20
; Sequence 20, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 20

```

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; LENGTH: 222
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-230-331-20

Query Match
Best Local Similarity 54.6%; Score 629.5; DB 14; Length 222;
Matches 121; Conservative 32; Mismatches 63; Indels 7; Gaps 3;

QY 1 MSVRASLSVSRTQTFVAPAAQI--RAKHTLPPLPYAYDALEPSISKEIMTLHHTKHQT 60
Db 1 MLSRAACST--SRLVLPALSVLGRQKHSPLDYPYDYGALPHEPHINAQIMQLHHSKHAAY 59

QY 61 NGLNAAEESYSAAGVKEDVLTVKLSALKFNGGHHNSLFWKQLAPYGSSEATLSEGP 120
Db 60 NNUNVAEKYREALEKGDVTAQIALQPAKFGGHHNSLFWKQLAPYGSSEATLSEGP 116

QY 121 LKKAIESFGSFAPKKKNADTAAGVQSGGWLGLNPLTKKLEVTTTANQDPL---LTH 177
Db 117 LLEAKRDFGSFAKFEKLTAVSVGVQSGGWLGLNPLTKKLEVTTTANQDPLQGT 176

QY 178 IPIGVDIWEHAFYLYQKNVDPYLAAVSVINYKEAEARLQA 220
Db 177 IPLGIDWEHAYLYQKNVRPDLKAIWNVINWENVTARYTA 219

RESULT 8
US-10-230-331-19
; Sequence 19, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 19
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-331-19

Query Match
Best Local Similarity 53.6%; Score 618; DB 14; Length 222;
Matches 115; Conservative 30; Mismatches 67; Indels 6; Gaps 2;

QY 6 SLSSVSRTQTFVAPAAQI--RAKHTLPPLPYAYDALEPSISKEIMTLHHTKHQT 65
Db 5 AVCGTSRQLAPALGVLSGRQKHSPLDYPYDYGALPHEPHINAQIMQLHHSKHAAYVNLNV 64

QY 66 ABEESYSAAGVKEDVLTVKLSALKFNGGHHNSLFWKQLAPYGSSEATLSEGPLKKA 125
Db 65 TEEKYQBALAKGDVTAQIALQPAKFGGHHNSLFWKQLAPYGSSEATLSEGPLKKA 121

QY 126 EESFGSFAPKKKNADTAAGVQSGGWLGLNPLTKKLEVTTTANQDPL---LTHPIIG 182
Db 122 KRDFGSFDFKFEKLTAAASVGVQSGGWLGLNPLTKKLEVTTTANQDPLQGT 181

QY 183 VDIWEHAFYLYQKNVDPYLAAVSVINYKEAEARLQA 220
Db 182 IDWWEHAYLYQKNVRPDLKAIWNVINWENVTARYMA 219

RESULT 9
US-10-424-599-233245
; Sequence 233245, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J

```


; APPLICANT: Jung, Vincent
 ; APPLICANT: Kretzmer, Keith A
 ; APPLICANT: Laccetti, Lucille B.
 ; APPLICANT: Lai, Chao-Qiang
 ; APPLICANT: Lee, Gary
 ; APPLICANT: Lin, Jie-Yi
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Lu, Bin
 ; APPLICANT: Luethy, Michael M.
 ; APPLICANT: Lund, Adrian
 ; APPLICANT: Madson, Linda L.
 ; APPLICANT: Malloy, Kathleen A.
 ; APPLICANT: McKiel, Christine L.
 ; APPLICANT: Miller, Philip W.
 ; APPLICANT: Padmavathi, Manchikanti
 ; APPLICANT: Parnell, Laurence D.
 ; APPLICANT: Start, William G.
 ; APPLICANT: Tennesen, Dan
 ; APPLICANT: Vidya, K.R.
 ; APPLICANT: Wang, Haiyun
 ; APPLICANT: Xin, Zhanguo
 ; APPLICANT: Xu, Nanfei
 ; APPLICANT: Yang, Chunzhi
 ; APPLICANT: Zeng, Xiaoping
 ; APPLICANT: Zhang, Qiang
 ; APPLICANT: Zhao, Yajuan
 ; APPLICANT: Zhou, Li
 ; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
 ; FILE REFERENCE: 38-15(52796)B
 ; CURRENT APPLICATION NUMBER: US/10/310,154
 ; CURRENT FILING DATE: 2002-12-04
 ; PRIOR APPLICATION NUMBER: 60/337,358
 ; PRIOR FILING DATE: 2001-12-04
 ; NUMBER OF SEQ ID NOS: 736
 ; SEQ ID NO 662
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; US-10-310-154-662

Query Match 51.1%; Score 589; DB 15; Length 233;
 Best Local Similarity 52.98; Pred. No. 4.2e-54;
 Matches 119; Conservative 30; Mismatches 64; Indels 12; Gaps 4;

QY	1	MSVRASLSSVSRTQF-----VAPAAFOIRAKHT--LPELPVAYDALEPPSISKEITMLHHT	53
DB	1	MALR-TLAKNALSFALGGAARPSAASAGVTTVTVALEDLSYDFGALEPAISGEIMRLHHQ	59
QY	54	KHQTQYNGLNABESYSAAVGKEDVLTVQKLSALKFNGGGHINHSFLFWKNLAPYSEE	113
DB	60	KHATYVANYNKALEQLDAAAVAKGDAVAVQLQGAIKFNGGGHVHNSIFWKNLKPISGG	119
QY	114	ATLSEGPLKKAIEESFGSPFAFKKNVADTAAVQSGSGWGLGNPLTKKLEVVITANQDP	173
DB	120	GEPPHGKLGWAIDEDFGSFALVKRMNAEGALQSGGWVWALDKEAKKL SVETTANQDP	179
QY	174	LLTH-----IPILGVDIWEHAFYIQYKNVKDYLAAVWSVINYKEA	214
DB	180	LVTGASLVPLLDIGDWEHAFYIQYKNVREDYLNINWKNWNYA	224

RESULT 13
 US-10-230-331-26
 ; Sequence 26, Application US/10230331
 ; Publication No. US20030157513A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RAJASEKHARAN, Ram
 ; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
 ; FILE REFERENCE: 110522
 ; CURRENT APPLICATION NUMBER: US/10/230,331
 ; CURRENT FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/315,757
 ; PRIOR FILING DATE: 2001-08-30

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OM protein - protein search, using sw model

Run on: March 30, 2004, 17:09:18 ; Search time 45 seconds
(without alignments)
1556.556 Million cell updates/sec

Title: US-09-727-855B-5
Perfect score: 1153
Sequence: 1 MSVRSLSSVSRTQTFVAPAA.....AAVMSVINYKEAEARLQAAL 222

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25.*

- 1: sp.archaea.*
- 2: sp.bacteria.*
- 3: sp.fungi.*
- 4: sp.human.*
- 5: sp.invertebrate.*
- 6: sp.mammal.*
- 7: sp.mhc.*
- 8: sp.organelle.*
- 9: sp.phage.*
- 10: sp.plant.*
- 11: sp.rodent.*
- 12: sp.virus.*
- 13: sp.vertebrate.*
- 14: sp.unclassified.*
- 15: sp.rviro.*
- 16: sp.bacterioph.*
- 17: sp.archaeop.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	751.5	65.2	206	3 Q96W28	Q96W28 phanerochaete
2	739.5	64.1	206	3 Q97773	Q97773 paxillus in
3	644.5	55.9	224	13 Q90Y34	Q90Y34 gallus gall
4	643.5	55.8	224	13 Q9DDJ1	Q9DDJ1 gallus gall
5	637.5	55.3	224	13 Q802D9	Q802D9 melopsittac
6	625.5	54.2	218	5 Q9NB66	Q9NB66 callinectes
7	617	53.5	213	4 Q727M4	Q727M4 homo sapien
8	616	53.4	222	4 Q96EE6	Q96EE6 homo sapien
9	615	53.3	199	6 Q8HXP4	Q8HXP4 macaca fusc
10	615	53.3	199	6 Q8HXP3	Q8HXP3 macaca fusc
11	615	53.3	199	6 Q8HXP2	Q8HXP2 macaca mulla
12	614	53.3	210	4 Q727M6	Q727M6 homo sapien
13	614	53.3	218	5 Q7YXMS	Q7YXMS apis mellif
14	614	53.3	231	10 Q65324	Q65324 raphanus sa
15	612.5	53.1	237	10 Q9M532	Q9M532 euphorbia e
16	611	53.0	199	6 Q8HXP5	Q8HXP5 hylobates 1

17	610	52.9	199	6 Q8HXP7	Q8HXP7 pan troglod
18	610	52.9	199	6 Q8HXP6	Q8HXP6 pongo pygma
19	608	52.7	213	4 Q7Z7M7	Q7Z7M7 homo sapien
20	608	52.7	231	10 Q947R3	Q947R3 raphanus sa
21	607	52.6	209	4 Q7Z7M5	Q7Z7M5 homo sapien
22	606	52.6	231	10 Q8LEP0	Q8LEP0 arabidopsis
23	605	52.5	199	6 Q8HXP1	Q8HXP1 cebus apell
24	605	52.5	199	6 Q8HXP0	Q8HXP0 callithrix
25	604	52.4	220	5 Q8MUI6	Q8MUI6 trichinella
26	600	52.0	228	10 Q9SNM64	Q9SNM64 prunus pers
27	598	51.9	237	3 Q873M4	Q873M4 malassezia
28	596.5	51.7	224	10 Q9FY33	Q9FY33 digitalis 1
29	596	51.7	226	10 Q84V26	Q84V26 avicennia m
30	595	51.7	231	10 Q96185	Q96185 triticum ae
31	590.5	51.2	231	10 Q43121	Q43121 oryza sativ
32	590.5	51.2	231	10 Q43803	Q43803 oryza sativ
33	587	50.9	231	10 P93606	P93606 triticum ae
34	584	50.7	235	10 Q43273	Q43273 zea mays (m
35	581	50.4	205	10 Q9STB5	Q9STB5 hevea bras
36	581	50.4	205	10 Q9FSJ2	Q9FSJ2 hevea bras
37	574	49.8	234	10 Q84W70	Q84W70 arabidopsis
38	574	49.8	240	10 Q82584	Q82584 zantedesch
39	574	49.8	241	10 Q9LYK8	Q9LYK8 arabidopsis
40	571.5	49.6	216	10 Q9FY32	Q9FY32 digitalis 1
41	570.5	49.5	224	10 Q82571	Q82571 triticum ae
42	566.5	49.1	230	3 Q874B1	Q874B1 cordyceps m
43	565	49.0	207	3 Q877B6	Q877B6 aspergillus
44	556.5	48.3	142	3 Q92464	Q92464 ganoderma t
45	555.5	48.2	142	3 Q92425	Q92425 ganoderma 1

ALIGNMENTS

RESULT 1

Q96W28	ID	Q96W28	PRELIMINARY;	PRT;	206 AA.
AC	Q96W28;				
DT	01-DEC-2001	(TREMREL. 19, Created)			
DT	01-DEC-2001	(TREMREL. 19, Last sequence update)			
DT	01-OCT-2003	(TREMREL. 25, Last annotation update)			
DE	Manganese superoxide dismutase (EC 1.15.1.1) (Superoxide dismutase [Mn/Fe]).				
DE	MNSODL				
OS	Phanerochaete chrysosporium.				
OC	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;				
OC	Aphyllophorales; Corticiales; Phanerochaete.				
OX	NCBI_TaxID=5306;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BKM-F-1767;				
RA	Dorosetz C.G., Goldberg D., Belinky P.A., Rothschild N., Krinfeld B., Kalati O., Burger M.;				
RT	"The manganese superoxide dismutase of Phanerochaete chrysosporium: its function, expression and gene structure.";				
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.				
CC	-!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELL AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).				
CC	-!- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).				
CC	-!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE FAMILY.				
DR	EMBL;	AF389395;	AAK82369.1;	--	
DR	GO;	GO:0004785;	Fcopper, zinc superoxide dismutase activity;	IEA.	
DR	GO;	GO:0008382;	Firon superoxide dismutase activity;	IEA.	
DR	GO;	GO:0008383;	Fmanganese superoxide dismutase activity;	IEA.	
DR	GO;	GO:0046872;	Fmetal ion binding;	IEA.	
DR	GO;	GO:0016954;	Fnickel superoxide dismutase activity;	IEA.	
DR	GO;	GO:0014491;	Foxidoreductase activity;	IEA.	
DR	GO;	GO:0006801;	Fsuperoxide metabolism;	IEA.	
DR	InterPro;	IPR001189;	SODismutase.		
DR	Pfam;	PF00081;	sofde; 1.		
DR	Pfam;	PF02777;	sofde.C; 1.		
DR	PRINTS;	PR01703;	MNSODISMUTASE.		

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DR ProDom: PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
KW Oxidoreductase.
SQ SEQUENCE 206 AA; 22860 MW; 63625CCFBD44A290 CRC64;

Query Match
  65.2%; Score 751.5; DB 3; Length 206;
Best Local Similarity 69.8%; Pred. No. 4.2e-60;
Matches 141; Conservative 25; Mismatches 27; Indels 9; Gaps 3;

QY 26 KHTLPPLPYADALEPSISKEIMTLHTKHQHTVYVGNLNAEESYS-AAVGKEDVLTVQVK 84
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 QHTLPPLPYADALEPYSVQIIMTLHHKHQHTVVTALNAEVSYAKTATPE---RIA 59
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 85 LQSALKFNGGGHINHSFWKNLAPVGSER---EATLSEGLPKKAIESFGSFEAFKKFKN 140
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 LQAALRENGGGHINHSFWKNLAPVGSER---EATLSEGLPKKAIESFGSFEAFKKFKN 119
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 141 ADTAAVQSGWGLGNPLTKKLEVTITANODPLLTHPIIGVDIWEHAFYLYQVKNVKPD 200
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 AATAAQSGWGLGNPLTKKLEVTITANODPLLTHPIIGVDIWEHAFYLYQVKNVKPD 179
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 201 YLAAVWSVINYKEAEARLQAL 222
   ||:|||||:|||||:
Db 180 YLNAINVINFEEAKRYLEAV 201
   ||:|||||:|||||:

RESULT 2
QY9Y773 PRELIMINARY; PRT; 206 AA.
ID Q9Y773 AC Q9Y773
DT 01-DEC-2001 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Manganese-superoxide dismutase (EC 1.15.1.1) (Superoxide dismutase
DE (Mn/Fel)).
DE NCBI_TaxID=71150;
GN MNSOD.
OS Paxillus involutus.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Boletales; Paxillineae; Paxillaceae; Paxillus.
OX NCBI_TaxID=71150;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 200175;
RA Jacob C., Courbot M., Botton B., Chalot M.;
RT "Cloning and sequencing of a full-length cDNA encoding the manganese
RT superoxide dismutase precursor of the ectomycorrhizal fungus, Paxillus
RT involutus."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR EMBL; AF114848; AAD25353.1; -.
DR HSP; P04179; IABM.
DR GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.
DR GO; GO:0008382; F:iron superoxide dismutase activity; IEA.
DR GO; GO:0008383; F:manganese superoxide dismutase activity; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0016954; F:nickel superoxide dismutase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006801; P:superoxide metabolism; IEA.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR Pfam; PF02777; sodfe_C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
KW Oxidoreductase.
SQ SEQUENCE 206 AA; 22696 MW; 7F1C6E51FF1AE0F5 CRC64;

Query Match
  64.1%; Score 739.5; DB 3; Length 206;
Best Local Similarity 69.3%; Pred. No. 5.2e-59;
Matches 123; Conservative 30; Mismatches 64; Indels 7; Gaps 3;

QY 1 MSVRASLSVSRTFVAFAAFOI-RAKHTLPPLPYADALEPSISKEIMTLHTKHQY 59
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MLCRLASGRSRAALVAPLGCVAKQHTLPDLPDYGALEPHISAEIMQLHSHKHAY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 VGNLNAEESYSAAVGKEDVLTVQVKLQSALKFNGGGHINHSFWKNLAPVGSER---RIA 119
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 VNNLVNTEKYEALAKGVDVTAQVSLQPALKNGGGHINHTILWTLNLSPPSGGE---PKG 117
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 120 PLKKAIESFGSFEAFKKFKNADTAAVQSGWGLGNPLTKKLEVTITANODPLLTHPIIGVDIWEHAFYLYQVKNVKPD 176
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 118 ELMEAIKRDGSPANFEKLTAVSVGQSGWGLYNKEQRLQIAACANQDPLQGTG 177
QY 177 HIPLIGVDIWEHAFYLOYNKVPDYLAAYVMSVINYKEAEARLOA 220
Db 178 LIPLIGDIDWEHAYFYLOYNKVPDYLAAYVMSVINYKEAEARLOA 221

RESULT 4

Q9DDJ1 PRELIMINARY; PRT; 224 AA.
AC Q9DDJ1 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Manganese-containing superoxide dismutase precursor (EC 1.15.1.1)
DE (Superoxide dismutase [Mn/Fe]).
GN MNSOD.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Bu Y.O., Luo X.G., Li S.F., Lu C., Li Y.W., Kuang X., Liu B., Li J.F.,
RA Yu S.X.;
RT "Cloning and Sequence Analysis of Manganese-containing Superoxide
Dismutase (MNSOD) cDNA of Chicken."
RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
FAMILY.
DR EMBL; AF323270; AAG46055.1; -.
DR HSP; P04179; IABM.
DR GO; GO:0004785; F.copper, zinc superoxide dismutase activity; IEA.
DR GO; GO:0008382; F.iron superoxide dismutase activity; IEA.
DR GO; GO:0008383; F.manganese superoxide dismutase activity; IEA.
DR GO; GO:0046872; F.metal ion binding; IEA.
DR GO; GO:0016954; F.nickel superoxide dismutase activity; IEA.
DR GO; GO:0016491; F.oxidoreductase activity; IEA.
DR GO; GO:0006801; P.superoxide metabolism; IEA.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR Pfam; PF02777; sodfe; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
KW Oxidoreductase; Signal.
FT SIGNAL 1 26
FT CHAIN 27 224
FT POTENTIAL.
FT MANGANESE-CONTAINING SUPEROXIDE
FT DISMUTASE.
SQ SEQUENCE 224 AA; 24946 MW; 1192114C7266687F CRC64;

Query Match 55.8%; Score 643.5; DB 13; Length 224;

Best Local Similarity 54.9%; Pred. No. 3e-50;

Matches 123; Conservative 28; Mismatches 66; Indels 7; Gaps 3;

QY 1 MSVRASLSVSRQTFVAP-AAFQIRAKHTLPPELAYDALEPSISKEIMTLHHTKHQTY 59
Db 1 MLCRLASGRSAALVAPWGCLVARQKHTLPDLPYDYGALPHISAEIMQLHSHKHATY 60
QY 60 VNLGNAEESYSAAGKEDVLTVQLQSKALFNGGHHNSLFWKMLAPYGSSEATLSG 119
Db 61 VNNLVNTEKYKEALAKGDTVQVSLQPKALFNGGHHNSLFWKMLAPYGSSEATLSG 117
QY 120 PLKKAIEESFGFEAFKKFNADTAAVQSGWGLYNKEQRLQIAACANQDPLQGTG 176
Db 118 ELMEAIKRDGSPANFEKLTAVSVGQSGWGLYNKEQRLQIAACANQDPLQGTG 177

QY 177 HIPLIGVDIWEHAFYLOYNKVPDYLAAYVMSVINYKEAEARLOA 220
Db 178 LIPLIGDIDWEHAYFYLOYNKVPDYLAAYVMSVINYKEAEARLOA 221

RESULT 5

Q802D9 PRELIMINARY; PRT; 224 AA.
AC Q802D9 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Mn superoxide dismutase.
GN SOD2
OS Melospittacus undulatus (Buderigar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Psittaciformes; Psittacidae;
OC Melospittacus.
OX NCBI_TaxID=13146;
RN [1]
RP SEQUENCE FROM N.A.
RA Austad S.N., Carlberg K.;
RT "Melospittacus undulatus Mn superoxide dismutase (SOD2) gene."
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY241394; AAO72712.1; -.
DR GO; GO:0046872; F.metal ion binding; IEA.
DR GO; GO:0004784; F.superoxide dismutase activity; IEA.
DR GO; GO:0006801; P.superoxide metabolism; IEA.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR Pfam; PF02777; sodfe; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
SQ SEQUENCE 224 AA; 24704 MW; F45DA30D58501D40 CRC64;

Query Match 55.3%; Score 637.5; DB 13; Length 224;

Best Local Similarity 56.4%; Pred. No. 1e-49;

Matches 124; Conservative 25; Mismatches 62; Indels 9; Gaps 4;

QY 7 LSSVRQT--FVAP-AAFQIRAKHTLPPELAYDALEPSISKEIMTLHHTKHQTYVNGL 63
Db 5 LSSAGRSSVKKVAPLGLASQKHTLPDLPYDYGALPHISAEIMQLHSHKHATVNNL 64
QY 64 NAAEESYSAAGKEDVLTVQLQSKALFNGGHHNSLFWKMLAPYGSSEATLSGPKK 123
Db 65 NVAEEKYKEALAKGDTVQVSLQPKALFNGGHHNSLFWKMLAPYGSSEATLSGPKK 121
QY 124 AJEESFGFEAFKKFNADTAAVQSGWGLYNKEQRLQIAACANQDPLQGTG 180
Db 122 AJKRDGSPANFEKLTAVSVGQSGWGLYNKEQRLQIAACANQDPLQGTG 181
QY 181 IGVDIWEHAFYLOYNKVPDYLAAYVMSVINYKEAEARLOA 220
Db 182 LGIDWEHAYFYLOYNKVPDYLAAYVMSVINYKEAEARLOA 221

RESULT 6

Q9NB66 PRELIMINARY; PRT; 218 AA.
AC Q9NB66 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Mitochondrial manganese superoxide dismutase precursor (EC 1.15.1.1)
DE (Superoxide dismutase [Mn/Fe]).
OS Callinectes sapidus (Blue crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Portunoidae; Portunidae; Callinectes.
OX NCBI_TaxID=6763;
RN [1]
RP SEQUENCE FROM N.A.


```
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
KW Hypothetical protein; Oxidoreductase.
SQ SEQUENCE 222 AA; 24750 MW; CA047D7900AE5905 CRC64;

Query Match
  53.4%; Score 616; DB 4; Length 222;
Best Local Similarity 53.2%; Pred. No. 9.1e-48;
Matches 117; Conservative 31; Mismatches 62; Indels 10; Gaps 4;

QY 6 SLSSVSRQTFVAPAAFI--RAKHTLPDPYDALEPSISKEIMTLHTKHQTYVNGL 63
DQ :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 5 AVCGTSRQ--LAPVLGYSRQKSLPDPYDYGALPHINAQIMQLHSHKHAAYVNNL 62
QY 64 NAAEESYGAAGKEDVLTQVQLQSALKFNGGGHINHSFWKNLAPYGEATLSEGLPKK 123
DQ :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 63 NTEKYQALAKGVDTAQIALQPALKFGGGHINHSIFWNLSPNGGGE---PKGELLE 119
QY 124 AIEESFGFEAFKKFNADTAAVQSGGWLGLNPLTKKLEVTITANODPL---LTHIP 180
DQ :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 120 AIKRDGFGDFKFKELTAASVGVQSGGWLGFNKRGHQLQAACPNQDPLQGTGLIPL 179
QY 181 IGVDIWEHAFYLYQKNVDPDYLAADVSVINYKEAEARLQA 220
DQ :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 180 LGIDWEHAYLYQKNVREDYLYKAINVINWENVTERYMA 219

RESULT 9
QHXKP4 PRELIMINARY; PRT; 199 AA.
AC Q8HXP4;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mn-superoxide dismutase.
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22271545; PubMed=12383507;
RA Fukuhara R., Tezuka T., Kageyama T.;
RT "Structure, molecular evolution, and gene expression of primate
RT superoxide dismutases.";
RL Gene 296:99-109 (2002).
DR EMBL; AB087278; BAC20356.1; -.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004784; F:superoxide dismutase activity; IEA.
DR GO; GO:0006801; P:superoxide metabolism; IEA.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
SQ SEQUENCE 199 AA; 22340 MW; 43B9CBE138C7E563 CRC64;

Query Match
  53.3%; Score 615; DB 6; Length 199;
Best Local Similarity 56.6%; Pred. No. 9.6e-48;
Matches 112; Conservative 27; Mismatches 53; Indels 6; Gaps 2;

QY 26 KHTLPDPYDALEPSISKEIMTLHTKHQTYVNGLNAAEESYSAAYGKEDVLTQVKL 85
DQ :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 2 KHSPLDLPYDYGALPHINAQIMQLHSHKHAAYVNNLVNTEKYQALAKGVDTAQIAL 61
QY 86 QSALKFNGGGHINHSFWKNLAPYGEATLSEGLPKKAEESFGFEAFKKFNADTA 145
DQ :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 62 QPALKFNGGGHINHSIFWNLSPNGGGE---PKGELLEAIKRDGFGFEKFKELTAASVG 118
QY 146 VQSGGWLGLNPLTKKLEVTITANODPL---LTHIPIGVDIWEHAFYLYQKNVDPDY 202
DQ :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 119 VQSGGWLGLFNKRQGLQAACPNQDPLQGTGLIPLIGIDWEHAYLYQKNVREDY 178
QY 203 AAVWSVINYKEAEARLQA 220
DQ :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 179 KAINVINWENVTERYMA 196

RESULT 11
QHXKP2 PRELIMINARY; PRT; 199 AA.
AC Q8HXP2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mn-superoxide dismutase.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
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```
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
KW Hypothetical protein; Oxidoreductase.
SQ SEQUENCE 222 AA; 24750 MW; CA047D7900AE5905 CRC64;

Query Match
  53.4%; Score 616; DB 4; Length 222;
Best Local Similarity 53.2%; Pred. No. 9.1e-48;
Matches 117; Conservative 31; Mismatches 62; Indels 10; Gaps 4;

QY 6 SLSSVSRQTFVAPAAFI--RAKHTLPDPYDALEPSISKEIMTLHTKHQTYVNGL 63
DQ :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 5 AVCGTSRQ--LAPVLGYSRQKSLPDPYDYGALPHINAQIMQLHSHKHAAYVNNL 62
QY 64 NAAEESYGAAGKEDVLTQVQLQSALKFNGGGHINHSFWKNLAPYGEATLSEGLPKK 123
DQ :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 63 NTEKYQALAKGVDTAQIALQPALKFGGGHINHSIFWNLSPNGGGE---PKGELLE 119
QY 124 AIEESFGFEAFKKFNADTAAVQSGGWLGLNPLTKKLEVTITANODPL---LTHIP 180
DQ :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 120 AIKRDGFGDFKFKELTAASVGVQSGGWLGFNKRGHQLQAACPNQDPLQGTGLIPL 179
QY 181 IGVDIWEHAFYLYQKNVDPDYLAADVSVINYKEAEARLQA 220
DQ :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 180 LGIDWEHAYLYQKNVREDYLYKAINVINWENVTERYMA 219

RESULT 9
QHXKP4 PRELIMINARY; PRT; 199 AA.
AC Q8HXP4;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mn-superoxide dismutase.
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22271545; PubMed=12383507;
RA Fukuhara R., Tezuka T., Kageyama T.;
RT "Structure, molecular evolution, and gene expression of primate
RT superoxide dismutases.";
RL Gene 296:99-109 (2002).
DR EMBL; AB087277; BAC20356.1; -.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004784; F:superoxide dismutase activity; IEA.
DR GO; GO:0006801; P:superoxide metabolism; IEA.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
SQ SEQUENCE 199 AA; 22340 MW; 43B9CBE138C7E563 CRC64;

Query Match
  53.3%; Score 615; DB 6; Length 199;
Best Local Similarity 56.6%; Pred. No. 9.6e-48;
Matches 112; Conservative 27; Mismatches 53; Indels 6; Gaps 2;

QY 26 KHTLPDPYDALEPSISKEIMTLHTKHQTYVNGLNAAEESYSAAYGKEDVLTQVKL 85
DQ :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 2 KHSPLDLPYDYGALPHINAQIMQLHSHKHAAYVNNLVNTEKYQALAKGVDTAQIAL 61
QY 86 QSALKFNGGGHINHSFWKNLAPYGEATLSEGLPKKAEESFGFEAFKKFNADTA 145
DQ :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 62 QPALKFNGGGHINHSIFWNLSPNGGGE---PKGELLEAIKRDGFGFEKFKELTAASVG 118
QY 146 VQSGGWLGLNPLTKKLEVTITANODPL---LTHIPIGVDIWEHAFYLYQKNVDPDY 202
DQ :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 119 VQSGGWLGLFNKRQGLQAACPNQDPLQGTGLIPLIGIDWEHAYLYQKNVREDY 178
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RP SEQUENCE FROM N.A.
RX MEDLINE=22271545; PubMed=12383507;
RA Fukuhara R., Teruka T., Kageyama T.;
RT "Structure, molecular evolution, and gene expression of primate
RL superoxide dismutases.";
RT Gene 296:99-109(2002).
DR EMBL: AB087279; BAC20358.1; -
DR GO: GO:0046872; F:metal ion binding; IEA.
DR GO: GO:0004784; F:superoxide dismutase activity; IEA.
DR GO: GO:0006801; P:superoxide metabolism; IEA.
DR InterPro: IPR001189; SODismutase.
DR Pfam: PF00081; sodfe; 1.
DR PRINTS: PR01703; MNSODISMUTASE.
DR ProDom: PD000475; SODismutase; 1.
DR PROSITE: PS00088; SOD_NW; 1.
SQ SEQUENCE 139 AA; 23340 MW; 43B9CBE138C7E563 CRC64;

Query Match 53.3%; Score 615; DB 6; Length 199;
Best Local Similarity 56.6%; Pred. No. 9.6e-48;
Matches 112; Conservative 27; Mismatches 53; Indels 6; Gaps 2;

Qy 26 KHTLPDPYDALEPSISKEIMTLHTKHHQTYVINGLNAAESYSAVAGKEDVLTQVKL 85
Db 2 KHSLEPDLPYDGALEPHINAQIMQLHSHKHAAYVNNLNVTEKYQELAKGDVTAQIAL 61
Qy 86 QSALKFNGGGHINSLFWKNLAPYGSSEATLSEGLKKAIESFGSFEAPKKFNADTAA 145
Db 62 QPALKFNGGGHINISIFWNLSPNGGE---PKGELLEAIKRDGSGFEKFEKLTAASVG 118
Qy 146 VQSGSGWGLNPLTKLELVTTANQDPL---LTHPIIGVDIWEHAFYLOKYNKPDYL 202
Db 119 VQSGSGWGLGFKNGRQGLQIAACPNQDPLQGTGTLPLGIDVWEHAYYLOKYNRPDY 178
Qy 203 AAVWSVINYKEAEARLQA 220
Db 179 KAIWNVINWENVTRYMA 196

RESULT 12
Q7Z7M6 PRELIMINARY; PRT; 210 AA.
AC Q7Z7M6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Manganese-containing superoxide dismutase (fragment).
GN SOD2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Mukhopadhyay S., Das S.K., Mukherjee S.;
RT "Differential Expression of Mn-SOD Gene in Normal and Cancerous Human
RT Mammary Epithelial Cells.";
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY280719; AAP34408.1; -
FT NON TER 1
FT NON TER 210
SQ SEQUENCE 210 AA; 23224 MW; 55B509814185894D CRC64;

Query Match 53.3%; Score 614; DB 4; Length 210;
Best Local Similarity 54.7%; Pred. No. 1.3e-47;
Matches 116; Conservative 31; Mismatches 55; Indels 10; Gaps 4;

Qy 6 SLSSVSQRTFVAPAAFI--RAKHTLPPELVAYDALEPSISKEIMTLHTKHHQTYVNG 63
Db 1 AVCGTSRQ--LAPALGYLSRQKSLPDLPYDGALEPHINAQIMQLHSHKHAAYVNNL 58
Qy 64 NAAESYSAVAGKEDVLTQVKLSALKFNGGGHINSLFWKNLAPYGSSEATLSEGLPK 123
Db 119 VQSGSGWGLGFKNGRQGLQIAACPNQDPLQGTGTLPLGIDVWEHAYYLOKYNRPDY 178

Db 59 NVTEKYQELAKGDVTAQIALQPALEKNGGGHINISIFWNLSPNGGE---PKGELLE 115
Qy 124 AIEESFGSFEAFKKFNADTAAVQSGSGWGLNPLTKLELVTTANQDPL---LTHPI 180
Db 116 AIKRDGSGFDKFEKLTAAVQSGSGWGLGFKNGRQGLQIAACPNQDPLQGTGTLPL 175
Qy 181 IGVDIWEHAFYLOKYNKPDYLAAVWSVINYK 212
Db 176 LGIDVWEHAYYLOKYNRPDYLKAIWNVINWE 207

RESULT 13
Q7YXMS PRELIMINARY; PRT; 218 AA.
AC Q7YXMS;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mn superoxide dismutase (fragment).
GN SOD2.
OS Apis mellifera ligustica (Common honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7469;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21923762; PubMed=11932240;
RA Whitfield C.W., Band M.R., Bonaldo M.F., Kumar C.G., Liu L.,
RA Pardinas J.R., Robertson H.M., Soares M.B., Robinson G.E.;
RT "Annotated expressed sequence tags and cDNA microarrays for studies of
RT brain and behavior in the honey bee.";
RL Genome Res. 12:555-566(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Corona M., Hughes K., Weaver D.B., Robinson G.E.;
RT "Longevity is not associated with high antioxidant gene expression in
RT honey bee queens.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY329356; AAP93582.1; -
FT NON TER 1
FT NON TER 218
SQ SEQUENCE 218 AA; 24567 MW; 6BB7ABB599E7C7E CRC64;

Query Match 53.3%; Score 614; DB 5; Length 218;
Best Local Similarity 51.6%; Pred. No. 1.3e-47;
Matches 116; Conservative 33; Mismatches 62; Indels 14; Gaps 3;

Qy 1 MSVRAISLSSVSQRTFVAPAAFIQIRAKHTLPPELVAYDALEPSISKEIMTLHTKHHQTYV 60
Db 3 VSYRIILPNTVKDTFT-----RTKHTLPDLPYDGALEPHIISAEIMQLHSHKHAATYV 55
Qy 61 NGLNAAESYSAVAGKEDVLTQVKLSALKFNGGGHINSLFWKNLAPYGSSEATLSEGP 120
Db 56 NNLNVAEEKKAEVAGKEDVNTQVLSFAIRKFGGGHINSLFWCNLSPNGK-----PDAA 111
Qy 121 LKKAIBESFGSFEAFKKFNADTAAVQSGSGWGLNPLTKLELVTTANQDPLTH--- 177
Db 112 LLNQIKKDFGSIEMKKELSENTIAIQSGSGWGLGYCQSKSLAIATCANQDPLQATTGL 171
Qy 178 IPTIGVDIWEHAFYLOKYNKPDYLAAVWSVINYKEAEARLQAAL 222
Db 172 IPLFGIDVWEHAYYLOKYNRPDYVKAIFDVVNNVNSRYKKA 216

RESULT 14
O65324 PRELIMINARY; PRT; 231 AA.
AC O65324;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Superoxide dismutase [Mn/Fe] (EC 1.15.1.1).
GN SOD.
```

OS Raphanus sativus (Radish).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids II; Brassicales; Brassicaceae; Raphanus.
 OX NCBI_TaxID=3726;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kwon S.-I., An C.-S.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR EMBL; AF061333; AAC15806.1; --.
 DR PIR; T08181; T08181.
 DR HSSP; P04179; IQNM.
 DR GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.
 DR GO; GO:0008383; F:iron superoxide dismutase activity; IEA.
 DR GO; GO:0008383; F:manganese superoxide dismutase activity; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0016954; F:nickel superoxide dismutase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006801; P:superoxide metabolism; IEA.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe_1.
 DR Pfam; PF02777; sodfe_C_1.
 DR PRINTS; PR01703; MNSODISMUTASE.
 DR PRODOM; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 231 AA; 25353 MW; DD709E5DBFF81A80 CRC64;
 Query Match 53.3%; Score 614; DB 10; Length 231;
 Best Local Similarity 57.5%; Pred. No. 1.5e-47;
 Matches 122; Conservative 20; Mismatches 54; Indels 16; Gaps 2;
 QY 7 LSSVSRQTFVAPAAQIRAKHTLPPLPYADALEPSISKEIMTLHTKHQHYVNGLNAA 66
 Db 23 LGSRSIQTF-----TLPLPDYSALEPAISGEIMQIHQKHQHYVNTYNNNA 70
 QY 67 EESYSAAGKEDVLTQVKLSALKFNGGGHINHSIFWKNLAPYGSBEATLSEGPLKKATE 126
 Db 71 LEQLQAVNKGDSASVVKLSAIFKNGGGHVNHSIFWKNLAPVKEGGGEPKSGSLGAID 130
 QY 127 EESGFEAPKKFNADTAAVQSGWGLGNPLTKKLEVTITANQDPLLTH-----IPIIG 182
 Db 131 TSFGSLEGLVKKMSAEGAAVQSGWVWLGIDKELKLVVDVTTANQDPLVTKGSLVPLVG 190
 QY 183 VDIWEHAFYLOQKNVKPDYLAAVWSVINKEA 214
 Db 191 IDVWEHAYFYLOQKNVRPDYLNKVNWKYA 222
 RESULT 15
 Q9M532 PRELIMINARY; PRT; 237 AA.
 AC Q9M532;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Manganese superoxide dismutase (EC 1.15.1.1) (Superoxide dismutase
 [Mn/Fel]).
 OS Euphorbia esula (Leafy spurge).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids I; Malpighiales; Euphorbiaceae; Euphorbioideae; Euphorbieae;
 CC Euphorbia.
 OX NCBI_TaxID=3993;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Underground adventitious buds;
 RA Anderson J.V., Horvath D.P.;

RT "Identification of mRNAs expressed in underground adventitious buds of
 RT Euphorbia esula (leafy spurge).";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR EMBL; AF242310; AAF65768.1; --.
 DR PIR; T50830; T50830.
 DR HSSP; P04179; IAB6.
 DR GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.
 DR GO; GO:0008383; F:iron superoxide dismutase activity; IEA.
 DR GO; GO:0008383; F:manganese superoxide dismutase activity; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0016954; F:nickel superoxide dismutase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006801; P:superoxide metabolism; IEA.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe_1.
 DR Pfam; PF02777; sodfe_C_1.
 DR PRINTS; PR01703; MNSODISMUTASE.
 DR PRODOM; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 237 AA; 26215 MW; 87EE25907EB702E0 CRC64;
 Query Match 53.1%; Score 612.5; DB 10; Length 237;
 Best Local Similarity 56.3%; Pred. No. 2.1e-47;
 Matches 120; Conservative 25; Mismatches 63; Indels 5; Gaps 2;
 QY 7 LSSVSRQTFVAPAAQIRAKHT--LPELPYADALEPSISKEIMTLHTKHQHYVNGLN 64
 Db 14 LASNSAKLVSGSAVQLRGKFTFSLPDYDYGALPAISGEIMQIHQKHQHYTTITNVN 73
 QY 65 AAEEYSAAVGGKEDVLTQVKLSALKFNGGGHINHSIFWKNLAPYGSBEATLSEGPLKKA 124
 Db 74 KALEQLHEATEKGDSDSTVVKLSAIFKNGGGHINHSIFWKNLAPVGGGGELPHGSLGWA 133
 QY 125 IEESFGFEAPKKFNADTAAVQSGWGLGNPLTKKLEVTITANQDPLLTH---IPII 181
 Db 134 IDKDFGSLEKLIQKNWTOGAAVQSGWVWLGLEKESKRLVWETTSNQDPLVTKGPLVPLV 193
 QY 182 GVDIWEHAFYLOQKNVKPDYLAAVWSVINKEA 214
 Db 194 GIDVWEHAYFYLOQKNVRPDYLNKVNWKYA 226
 Search completed: March 30, 2004, 17:10:21
 Job time : 48 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2004, 17:11:03 ; Search time 18 Seconds
(without alignments)
642.199 Million cell updates/sec

Title: US-09-727-855B-5
Perfect score: 1153
Sequence: 1 MSVRASLSVSQTTFVAPAA.....AAVWSVINYKEARLQAAL 222

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	748.5	64.9	200	1 SODM_GANMI	Q92429 ganoderma m
2	634.5	55.0	222	1 SODM_MOUSE	P07671 mus musculus
3	634.5	55.0	222	1 SODM_RAT	P07895 rattus norv
4	629.5	54.6	222	1 SODM_BOVIN	P41976 bos taurus
5	620	53.8	222	1 SODM_HUMAN	P04179 homo sapien
6	615.5	53.4	222	1 SODM_HORSE	Q9xs41 equus caball
7	615	53.3	198	1 SODM_MACFA	Q8hxp3 macaca fasc
8	615	53.3	198	1 SODM_MACFU	Q8hxp2 macaca mula
9	615	53.3	198	1 SODM_MACMU	Q8hxp5 hyllobates l
10	611	53.0	198	1 SODM_HYLLA	Q8hxp7 pan troglod
11	610	52.9	198	1 SODM_PANTR	Q8hxp6 pongo pygma
12	610	52.9	198	1 SODM_PONPY	Q81235 arabidopsis
13	606	52.6	231	1 SODM_ARATH	Q8hxp0 callithrix
14	605	52.5	198	1 SODM_CALJA	Q8hxp1 cebus apell
15	605	52.5	198	1 SODM_CEBAP	P49114 cavia porce
16	601	52.1	211	1 SODM_CAVPO	Q9sm64 prunus pers
17	600	52.0	228	1 SODM_DRUME	Q00637 drosophila
18	595.5	51.6	217	1 SODM_DROME	P35017 hevea bras
19	595	51.6	233	1 SODM_HVBR	P41982 oryctolagus
20	592	51.3	202	1 SODM_RABIT	P11796 nicotiana p
21	592	51.3	228	1 SODM_NICPL	Q43008 oryza sativ
22	590.5	51.2	231	1 SODM_ORYSA	P41980 zea mays (m
23	590	51.2	233	1 SODP_MAIZE	P09233 zea mays (m
24	586	50.8	235	1 SODM_MAIZE	P31161 caenorhabdi
25	584.5	50.7	221	1 SODM_CAEEL	Q92450 aspergillus
26	583.5	50.6	210	1 SODM_ASFFU	Q49066 capsicum an
27	582	50.5	228	1 SODM_CAPAN	P41977 caenorhabdi
28	572	49.6	218	1 SODN_CAEEL	P41978 zea mays (m
29	570.5	49.5	232	1 SODN_MAIZE	O75007 penicillium
30	567.5	49.2	210	1 SODM_PENCH	Q9uqx0 schizosacch
31	560	48.6	218	1 SODM_SCHPO	P41979 zea mays (m
32	558	48.4	233	1 SODO_MAIZE	P27084 pismus sativ
33	556.5	48.3	233	1 SODM_PEA	

34	556.5	48.3	245	1 SODM_NEUCR	Q9y783 neurospora
35	555.5	48.2	200	1 SODM_AGABI	Q9p4t6 agaricus bi
36	535.5	46.4	205	1 SODM_CHLMU	Q9pka0 chlamydia m
37	529.5	45.9	206	1 SODM_CHLTR	O84296 chlamydia t
38	529	45.9	224	1 SODM_CHAFE	O96347 charybdis f
39	514.5	44.6	207	1 SODM_CHLPN	O929c4 chlamydia p
40	511	44.3	203	1 SODM_BACAA	Q811w0 bacillus an
41	504.5	43.8	201	1 SODM_BACSU	P54375 bacillus su
42	503	43.6	203	1 SODM_XANCP	P53854 xanthomonas
43	496	43.0	203	1 SODM_BACCA	P28760 bacillus ca
44	495	42.9	203	1 SODM_BACST	P00449 bacillus st
45	492	42.7	202	1 SODM_LISMO	P28764 listeria mo

ALIGNMENTS

RESULT 1
SODM_GANMI
ID SODM_GANMI STANDARD; PRT; 200 AA.
AC Q92429; 1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
OS Ganoderma microsporium
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Ganodermataceae; Ganoderma.
OX NCBI_TaxID=34462;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BSH 0821;
RA Wang H.F.;
RL Thesis (1996), National Taiwan University, Taiwan.
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.

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EMBL; U56403; AAB07360.1; -;
EMBL; U56127; AAB16782.1; -;
HSSP; P04179; IAHM.
InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR Pfam; PF02777; sodfe.C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
DR Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
KW Transit peptide.
FT TRANSIT 1 ? MITOCHONDRION (POTENTIAL).
FT CHAIN ? 200 SUPEROXIDE DISMUTASE [MN].
FT METAL 27 27 MANGANESE (BY SIMILARITY).
FT METAL 72 72 MANGANESE (BY SIMILARITY).
FT METAL 161 161 MANGANESE (BY SIMILARITY).
FT METAL 165 165 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 200 AA; 22170 MW; E39DFC7E1708961F CRC64;

Query Match 64.9%; Score 748.5; DB 1; Length 200;
Best Local Similarity 71.6%; Pred. No. 1.2e-59;
Matches 141; Conservative 24; Mismatches 23; Indels 9; Gaps 3;

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QY 27 HTLPPEYDALPSPISKEIMTLHTKHQTYVNGLNAAESYS-AAVGKEDVLTQVKL 85
Db 3 HVLFDLPYANNALBPFFSQOIMELHKKHQTYSNLNAAEQAKASTPKS-----RIAL 58
QY 86 QSALKFNGGGHINSLFWKNIAPYGE-----EATLSEGLPKALIEBSFGSFEAPKXKFN 141
Db 59 QSALKFNGGGHINSLFWKNIAPAKSEKGGKNGALADGPKLSALEQNGWSVDNFIKEFNA 118
QY 142 DTAAVQSGWGLNGINLPTKKLEVTITANOPDLTHPIIGVDIWEHAFYLOYKXKVPDY 201
Db 119 TTAATQSGWGLNGINLPTKKLEVTITANOPDLTHPIIGVDIWEHAFYLOYKXKVPDY 178
QY 202 LAAVWSVINYKEAERL 218
Db 179 LAAIWINVINFKEAERL 195

RESULT 2
SODM_MOUSE STANDARD; PRT; 222 AA.
AC P09671; Q64670; Q8VEM5;
DT 01-MAR-1989 (Rel. 10, Created)
DT 15-JUL-1998 (Rel. 36, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
GN SOD2 OR SOD-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=87091590; PubMed=3797253;
RA Hallowell R.A., Mullenbach G.T., Stempien M.M., Bell G.I.;
RT "Sequence of a cDNA coding for mouse manganese superoxide dismutase.";
RL Nucleic Acids Res. 14:9539-9539(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c, and C3H;
RX MEDLINE=94010326; PubMed=8406027;
RA Sun Y., Heganyer G., Colburn N.M.;
RT "Sequence of manganese superoxide dismutase-encoding cDNAs from
multiple mouse organs.";
RL Gene 131:301-302(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95180711; PubMed=7875582;
RA Jones P.L., Kucera G., Gordon H.M., Boss J.M.;
RT "Cloning and characterization of the murine manganese superoxide
dismutase-encoding gene.";
RL Gene 153:155-161(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95337589; PubMed=7613035;
RA Disilvestre D., Kleiberger S.R., Johns J., Levitt R.C.;
RT "Structure and DNA sequence of the mouse MnSOD gene.";
RL Mamm. Genome 6:281-284(1995).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo, and Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriin L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

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RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.F.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
family.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X04972; CAA28645.1; -
DR EMBL; Z18857; CAA79308.1; -
DR EMBL; L35528; AAB60902.1; JOINED.
DR EMBL; L35526; AAB60902.1; JOINED.
DR EMBL; L35527; AAB60902.1; JOINED.
DR EMBL; S78846; AAB34899.1; -
DR EMBL; S78832; AAB34899.1; JOINED.
DR EMBL; S78842; AAB34899.1; JOINED.
DR EMBL; S78844; AAB34899.1; JOINED.
DR EMBL; AK002428; BAB22095.1; -
DR EMBL; AK002534; BAB22170.1; -
DR EMBL; AK012354; BAB28183.1; -
DR EMBL; BC010548; AAH10548.1; -
DR EMBL; BC018173; AAH18173.1; -
DR FIR; I57023; I57023.
DR HSSP; P04179; IABM.
DR SWISS-2DPAGE; P09671; MOUSE.
DR MGD; MGI:983352; Sod2.
DR GO; GO:0008383; P:manganese superoxide dismutase activity; IMP.
DR GO; GO:0006801; P:superoxide metabolism; IMP.
DR InterPro; IPR001189; SOD1dmutase.
DR Pfam; PF00081; sodfe; 1.

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DR Pfam; PF02777; sodfe C; 1.
 DR PRINTS; PR01703; MNSODISMUTASE.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD MN; 1.
 KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
 KW Transit peptide.
 KW TRANSIT 1 24 MITOCHONDRION.
 FT CHAIN 25 222 SUPEROXIDE DISMUTASE [MN].
 FT METAL 50 50 MANGANESE (BY SIMILARITY).
 FT METAL 98 98 MANGANESE (BY SIMILARITY).
 FT METAL 183 183 MANGANESE (BY SIMILARITY).
 FT METAL 187 187 MANGANESE (BY SIMILARITY).
 FT CONFLICT 5 5 A -> G (IN REF. 5; AAH18173).
 FT CONFLICT 18 18 G -> V (IN REF. 1).
 FT CONFLICT 138 138 V -> M (IN REF. 1 AND 3).
 SQ SEQUENCE 222 AA; 24603 MW; 9AE804C55A8357D9 CRC64;
 Query Match 55.0%; Score 634.5; DB 1; Length 222;
 Best Local Similarity 55.6%; Pred. No. 2e-49;
 Matches 124; Conservative 30; Mismatches 62; Indels 7; Gaps 3;
 QY 1 MSVRASLSVSRQTFVAPAAQFIRAKHTLPDLPVAYDALEPSISKETIMTLHHTKHQTVV 60
 Db 1 MLCRAACSTGRGLPVGAGAGS-RHKHSUPDLDPYDYGALPEPHINAQIMQLHSHKHAAYV 59
 QY 61 NGLNAAEESYSAAVGKEDVLTQVKLSALKFNGGGHINHSFLWKNLAPYGESEATLSEGP 120
 Db 60 NNLNATEEKYHEALAKGDVTTQVALQPAKFNGGGHINHTFTWNLSPKGGGE---PKGE 116
 QY 121 LKKAIESFGSFEAFKKFNADTAAGVGGSGWGLNPLTKKLEVTTTANQDPL---LTH 177
 Db 117 LLEAIKRDGFSFEKFEKLTAVSVGVGGSGWGLGNKEQGRQIAACSNQDPLQGTG 176
 QY 178 IPTIGVDIWEHAFYLOVKNKPDYLAAVWSVINYKEAEARLQA 220
 Db 177 IFLLGIDVWEHAYLYQKVRPDYLAAMVNVINWNTERYTA 219
 RESULT 3
 SODM RAT STANDARD; PRT; 222 AA.
 ID F07895;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
 GN SOD2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]_SEQUENCE FROM N.A.
 RP STRAIN=Sprague-Dawley; TISSUE=Liver;
 RC MEDLINE=88096516; PubMed=3697077;
 RA Ho Y.-S., Crapo J.D.;
 RT "Nucleotide sequences of cDNAs coding for rat manganese-containing superoxide dismutase."
 RL Nucleic Acids Res. 15:10070-10070(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=91159005; PubMed=2001291;
 RA Ho Y.-S., Howard A.J., Crapo J.D.;
 RT "Molecular structure of a functional rat gene for manganese-containing superoxide dismutase."
 RL Am. J. Respir. Cell Mol. Biol. 4:278-286(1991).
 CC -!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
 CC -!- SUBUNIT: Homotrimer.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.

CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase family.
 CC -----
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 CC -----
 CC EMBL; Y00497; CAA68549.1; -
 DR EMBL; X56600; CAA39937.1; -
 DR PIR; S21661; DSRTN.
 DR HSSP; P04179; IAEH.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.
 DR Pfam; PF02777; sodfe C; 1.
 DR PRINTS; PR01703; MNSODISMUTASE.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD MN; 1.
 KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
 KW Transit peptide.
 KW TRANSIT 1 24 MITOCHONDRION.
 FT CHAIN 25 222 SUPEROXIDE DISMUTASE [MN].
 FT METAL 50 50 MANGANESE (BY SIMILARITY).
 FT METAL 98 98 MANGANESE (BY SIMILARITY).
 FT METAL 183 183 MANGANESE (BY SIMILARITY).
 FT METAL 187 187 MANGANESE (BY SIMILARITY).
 FT CONFLICT 167 167 Q -> H (IN REF. 1).
 SQ SEQUENCE 222 AA; 24674 MW; 8CCC1E0E857B3138 CRC64;
 Query Match 55.0%; Score 634.5; DB 1; Length 222;
 Best Local Similarity 55.4%; Pred. No. 2e-49;
 Matches 123; Conservative 30; Mismatches 58; Indels 11; Gaps 4;
 QY 1 MSVRASLSVSRQTFVAPAAQFI--RAKHTLPDLPVAYDALEPSISKETIMTLHHTKHQ 58
 Db 1 MLCRAACSGRR--LGPAASTAGSRHKHSLDLPDYDYGALPEPHINAQIMQLHSHKHAT 57
 QY 59 YVNGLNAAEESYSAAVGKEDVLTQVKLSALKFNGGGHINHSFLWKNLAPYGESEATLS 118
 Db 58 YVNNLVNTEEKYHEALAKGDVTTQVALQPAKFNGGGHINHSIFWNLSPKGGGE---PK 114
 QY 119 GPLKKAIESFGSFEAFKKFNADTAAGVGGSGWGLNPLTKKLEVTTTANQDPL---L 175
 Db 115 GELLEAIKRDGFSFEKFEKLTAVSVGVGGSGWGLGNKEQGRQIAACSNQDPLQGT 174
 QY 176 THIPIIGVDIWEHAFYLOVKNKPDYLAAVWSVINYKEAEAR 217
 Db 175 GLIPLIGIDVWEHAYLYQKVRPDYLAAMVNVINWENVSR 216
 RESULT 4
 SODM BOVIN STANDARD; PRT; 222 AA.
 ID -SODM BOVIN
 AC P41376;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
 GN SOD2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]_SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=94121934; PubMed=8292376;
 RA Meyrick B., Magnuson M.A.;
 RT "Identification and functional characterization of the bovine

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RT  manganoous superoxide dismutase promoter.";
RL  Am. J. Respir. Cell Mol. Biol. 10:113-121(1994).
CC  -!- FUNCTION: Destroys radicals which are normally produced within the
CC  cells and which are toxic to biological systems.
CC  -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC  -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC  -!- SUBUNIT: Homotetramer (By similarity).
CC  -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC  -!- SIMILARITY: LOCATIONS: Mitochondrial matrix.
CC  -!- SIMILARITY: Locations to the iron/manganese superoxide dismutase
CC  family.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; L22092; AAA30655.1; ALT_INIT.
DR  EMBL; L22093; AAA30656.1; -.
DR  EMBL; S67818; AAC60522.2; -.
DR  EMBL; S67819; AAD14001.1; -.
DR  PIR; I51918; I51918.
DR  HSSP; P04179; IABM.
DR  InterPro: IPR001189; SODismutase.
DR  Pfam; PF00081; sodfe_1.
DR  Pfam; PF02777; sodfe_c1.
DR  PRINTS; PR01703; MNSCDSMTASE.
DR  ProDom; PD000475; SODismutase.
DR  PROSITE; PS00088; SOD MN; 1.
KW  Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
KW  transit peptide.
FT  TRANSIT 1 24 MITOCHONDRION (BY SIMILARITY).
FT  CHAIN 25 222 SUPEROXIDE DISMUTASE [MN].
FT  METAL 50 50 MANGANESE (BY SIMILARITY).
FT  METAL 98 98 MANGANESE (BY SIMILARITY).
FT  METAL 183 183 MANGANESE (BY SIMILARITY).
FT  METAL 187 187 MANGANESE (BY SIMILARITY).
FT  CONFLICT 8 8 S -> R (IN REF. 1; AAD14001).
FT  CONFLICT 90 90 F -> V (IN REF. 1; AAC60522).
SQ  SEQUENCE 222 AA; 24638 MW; 806CC3FCB1A74413 CRC64;

Query Match 54.6%; Score 629.5; DB 1; Length 222;
Best Local Similarity 54.3%; Pred. No. 5.5e-49;
Matches 121; Conservative 32; Mismatches 63; Indels 7; Gaps 3;

QY 1 MSVRASLSVSRTQTFVAPAAFOIRAKHTLPPELPAYDALEPSISKEIMTLHTKHQTVY 60
Db 1 MLSRAACST-SRRLVPALSVLSGRKHSPLPDLPYDYGALPHINAQIMQLHSHKHAAYV 59

QY 61 NGLNABESYSNAVGKEDVLTQVKLSALKFNGGGHINHSLEFWKMLAPYGSBEATLSEGP 120
Db 60 NNLNVAEEKYREALEKGDVTAQIALQPALKFNKGHHINHSIFWTLNLPNGGGE---PQGE 116

QY 121 LKKAITEESFGSFEAPKPKFNADTAQVSGSGWGLGNPLTKLEVTVTANQDPL---LTH 177
Db 117 LLEALIKRFSGFAKFEKLTATSVSGVGGSGWGLGNFNKFNKQGRLOIAACSNQDPLQGTGL 176

QY 178 IPIIGVDIWEHAFYLYQKNVKPDYLAADVMSVINYKEAEARLQA 220
Db 177 IPLLGLDVEHAFYLYQKNVRPDYLAIAWVNWENVTARYTA 219

RESULT 5
SODM HUMAN STANDARD; PRT; 222 AA.
AC P04179; P78434; Q16792; Q9P223;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
GN SOD2.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89076921; PubMed=2462451;
RA Wispe J.R., Clark J.C., Burhans M.S., Kropp K.E., Korfhagen T.R.,
RA Whitsett J.A.;
RT "Synthesis and processing of the precursor for human
RT manganese superoxide dismutase.";
RL Biochim. Biophys. Acta 994:30-36(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88067716; PubMed=3684581;
RA Beck Y., Oren R., Amit B., Levanon A., Gorecki M., Hartman J.R.;
RT "Human Mn superoxide dismutase cDNA sequence.";
RL Nucleic Acids Res. 15:9076-9076(1987).
RN [3]
RP SEQUENCE FROM N.A.; AND VARIANT VAL-16.
RX MEDLINE=88289364; PubMed=3399391;
RA Heckl K.;
RT "Isolation of cDNAs encoding human manganese superoxide dismutase.";
RL Nucleic Acids Res. 16:6224-6224(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RX MEDLINE=88152250; PubMed=2831093;
RA Ho Y.-S., Crapo J.D.;
RT "Isolation and characterization of complementary DNAs encoding human
RT manganese-containing superoxide dismutase.";
RL FEBS Lett. 229:256-260(1988).
RN [5]
RP SEQUENCE FROM N.A.
RX TISSUE=Colon;
RX MEDLINE=91105727; PubMed=1988135;
RA St Clair D.K., Holland J.C.;
RT "Complementary DNA encoding human colon cancer manganese superoxide
RT dismutase and the expression of its gene in human cells.";
RL Cancer Res. 51:939-943(1991).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=91027939; PubMed=1699607;
RA Church S.L.;
RT "Manganese superoxide dismutase: nucleotide and deduced amino acid
RT sequence of a cDNA encoding a new human transcript.";
RL Biochim. Biophys. Acta 1087:250-252(1990).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=95217333; PubMed=7702755;
RA Wan X.S., Devalaraja M.N., St Clair D.K.;
RT "Molecular structure and organization of the human manganese
RT superoxide dismutase gene.";
RL DNA Cell Biol. 13:1127-1136(1994).
RN [8]
RP SEQUENCE OF 25-222.
RX MEDLINE=85030346; PubMed=6386798;
RA Barra D., Schinina M.E., Simmaco M., Bannister J.V., Bannister W.H.,
RA Rotilio G., Bossa F.;
RT "The primary structure of human liver manganese superoxide
RT dismutase.";
RL J. Biol. Chem. 259:12595-12601(1984).
RN [9]
RP SEQUENCE OF 25-39.
RX TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RT 1994.";
RL Electrophoresis 15:1459-1465(1994).
RN [10]
RP SEQUENCE OF 25-39.
RX TISSUE=Heart;

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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1)
(Mn-SOD).
GN
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBT_TaxID=9796;
RN
[1]
SEQUENCE FROM N.A.
MEDLINE=99261591; PubMed=10331206;
RA Ishida N., Katayama Y., Sato F., Hasegawa T., Mukoyama H.;
RC TISSUE=Testis;
RT "The cDNA sequences of equine antioxidative enzyme genes Cu/Zn-SOD and
RL J. Vet. Med. Sci. 61:291-294(1999).
CC
-!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC
-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC
-!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC
-!- SUBUNIT: Homotrimer (By similarity).
CC
-!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC
-!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC
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CC or send an email to license@isb-sib.ch).
CC
EMBL; AB001693; BAA76922.1; -
DR HSP; P04179; IABM.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sofde; 1.
DR Pfam; PF02777; sofde; C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
KW Transit peptide.
FT TRANSIT 1 24 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 25 222 SUPEROXIDE DISMUTASE [MN].
FT METAL 50 50 MANGANESE (BY SIMILARITY).
FT METAL 98 98 MANGANESE (BY SIMILARITY).
FT METAL 183 183 MANGANESE (BY SIMILARITY).
FT METAL 187 187 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 222 AA; 24739 MW; 93A069481944E98C CRC64;

Query Match 53.4%; Score 615.5; DB 1; Length 222;
Best Local Similarity 52.9%; Pred. No. 9.8e-48;
Matches 118; Conservative 32; Mismatches 66; Indels 7; Gaps 3;

QY 1 MSVRASLSSVSRQTFVAPAAQIRAKHTLPELPYADALEPSISKEIMTLHHTKHQTYV 60
DB 1 MLCRAACST-SRKLVPALGSLGRQKSLPDLQYDYGALPEYINAIQMLHSHKHAAYV 59

61 NGLNAABESYAAVKGEDVLTQVKLQSKALFKNGGGHINSLFWKNLAPYSGEATLSBGP 120
DB 60 NNINLVTEKYQALAKGVDVTAQIALQPALFKNGGGHINHTFTWNLSPNGGGE---PKGK 116

121 LKKAIEESFGSPFAKFKFNADTAAGVSGWGLGNPLTKLEVTITANQDPL---LTH 177
DB 117 LLDLAKRDFGDFKFKELTAVSAGVQSGWGLGNQKQGLQVACPNQDPLQGTGL 176

178 IPIIGVDIWEHAFYLOQKNVPDYLAAVMSVINYKEAEARLQA 220
DB 177 IPIIGVDIWEHAFYLOQKNVPDYLAAVMSVINYKEAEARLQA 219

RESULT 7
SODM_MACFA STANDARD; PRT; 198 AA.
ID O8HXP3.
AC 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
GN SOD2.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBT_TaxID=9541;
RN
[1]
SEQUENCE FROM N.A.
MEDLINE=22271545; PubMed=12383507;
RA Fukuhara R., Tezuka T., Kageyama T.;
RT "Structure, molecular evolution, and gene expression of primate
RT superoxide dismutases.";
RL Gene 296:99-109(2002).
CC
-!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC
-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC
-!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC
-!- SUBUNIT: Homotrimer (By similarity).
CC
-!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC
-!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC
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CC or send an email to license@isb-sib.ch).
CC
EMBL; AB087278; BAC20357.1; ALT_INIT.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sofde; 1.
DR Pfam; PF02777; sofde; C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
FT METAL 26 26 MANGANESE (BY SIMILARITY).
FT METAL 74 74 MANGANESE (BY SIMILARITY).
FT METAL 159 159 MANGANESE (BY SIMILARITY).
FT METAL 163 163 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 198 AA; 22209 MW; FB4F6B063198E5CC CRC64;

Query Match 53.3%; Score 615; DB 1; Length 198;
Best Local Similarity 56.6%; Pred. No. 9.4e-48;
Matches 112; Conservative 27; Mismatches 53; Indels 6; Gaps 2;

QY 26 KHTLPYADALEPSISKEIMTLHHTKHQTYVNGLNAAEESYAAVKGEDVLTQVKL 85
DB 1 KHSLEPDLPYDGALEPHINAIQMLHSHKHAAYNNINLVTEKYQALAKGVDVTAQIAL 60

86 QSKALFKNGGGHINSLFWKNLAPYSGEATLSBGLPKKAIESFGSPFAKFKFNADTA 145
DB 61 QPALFKNGGGHINSLFWKNLAPYSGEATLSBGLPKKAIESFGSPFAKFKFNADTA 117

146 VQSGWGLGNPLTKLEVTITANQDPL---LTHPIIGVDIWEHAFYLOQKNVPDYLA 202
DB 118 VQSGWGLGNPLTKLEVTITANQDPL---LTHPIIGVDIWEHAFYLOQKNVPDYLA 177

203 AAWSVINYKEAEARLQA 220
DB 178 KAIWNVINWENVTERYMA 195
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RESULT 8
SODM_MACFU          STANDARD;          PRT;    198 AA.
ID  Q8HXP4;
AC  Q8HXP2;
DT  15-MAR-2004 (Rel. 43, Created)
DT  15-MAR-2004 (Rel. 43, Last sequence update)
DT  15-MAR-2004 (Rel. 43, Last annotation update)
DE  Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
GN  SOD2.
OS  Macaca fuscata fuscata (Japanese macaque).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC  Cercopithecinae; Macaca.
OX  NCBI_TaxID=9543;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=22271545; PubMed=12383507;
RA  Fukuhara R., Tezuka T., Kageyama T.;
RT  "Structure, molecular evolution, and gene expression of primate
RT  superoxide dismutases.";
RL  Gene 296:99-109(2002).
CC  -!- FUNCTION: Destroys radicals which are normally produced within the
CC  cells and which are toxic to biological systems.
CC  -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC  -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC  -!- SUBUNIT: Homotetramer (By similarity).
CC  -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC  -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC  family.
CC
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CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC
CC  EMBL; AB087277; BAC20356.1; ALT_INIT.
CC  InterPro; IPR001189; SODismutase.
CC  Pfam; PF00081; sodfe; 1.
CC  PRINTS; PR01703; MNSODISMASE.
CC  ProDom; PD000475; SODismutase; 1.
CC  PROSITE; PS00088; SOD_MN; 1.
KW  Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
FT  METAL 26 26 MANGANESE (BY SIMILARITY).
FT  METAL 74 74 MANGANESE (BY SIMILARITY).
FT  METAL 159 159 MANGANESE (BY SIMILARITY).
FT  METAL 163 163 MANGANESE (BY SIMILARITY).
SQ  SEQUENCE 198 AA; 22209 MW; FB4F6B063198E5CC CRC64;

Query Match          53.3%; Score 615; DB 1; Length 198;
Best Local Similarity 56.6%; Pred. No. 9.4e-48;
Matches 112; Conservative 27; Mismatches 53; Indels 6; Gaps 2;

QY  26 KHTLPPLPAYDALEPSISKETMTLHTKHQTYVNGLNAAEESYSAAYGKEDVLTQVKL 85
DB  1 KHSPLDLPDYDGALEPHINAQIMQLHSHKHAAYVNNLVNTEKYQEALAKGDTVTAQIAL 60

QY  86 QSALKFNGGGCHNHSIFWKNLAPYGSSEATLSGPKLKAEESFGSFEAFKKFNADTAA 145
DB  61 QPALKFNGGGCHNHSIFWNLSPNGGGE---PKGELLEAIKRDGSGFEKFKLTAAVSG 117

QY  146 VQSGGWMGLNPLTKKLEVTITANQDPL---LTHPIIGVDIWEHAFYLYQKNVXPDYL 202
DB  118 VQSGGWMGLGNKRGKQQLQIAACPNQDPLQGTGTLPLIGIDVWEHAFYLYQKNVXPDYL 177

QY  203 AAVWSVINYKEAEARLQA 220
DB  178 KAIWNVINWENVTRYMA 195

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RESULT 9
SODM_MACMU          STANDARD;          PRT;    198 AA.
ID  Q8HXP2;
AC  Q8HXP2;
DT  15-MAR-2004 (Rel. 43, Created)
DT  15-MAR-2004 (Rel. 43, Last sequence update)
DT  15-MAR-2004 (Rel. 43, Last annotation update)
DE  Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
GN  SOD2.
OS  Macaca mulatta (Rhesus macaque).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC  Cercopithecinae; Macaca.
OX  NCBI_TaxID=9544;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=22271545; PubMed=12383507;
RA  Fukuhara R., Tezuka T., Kageyama T.;
RT  "Structure, molecular evolution, and gene expression of primate
RT  superoxide dismutases.";
RL  Gene 296:99-109(2002).
CC  -!- FUNCTION: Destroys radicals which are normally produced within the
CC  cells and which are toxic to biological systems.
CC  -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC  -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC  -!- SUBUNIT: Homotetramer (By similarity).
CC  -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC  -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC  family.
CC
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC
CC  EMBL; AB087279; BAC20358.1; ALT_INIT.
CC  InterPro; IPR001189; SODismutase.
CC  Pfam; PF00081; sodfe; 1.
CC  PRINTS; PR01703; MNSODISMASE.
CC  ProDom; PD000475; SODismutase; 1.
CC  PROSITE; PS00088; SOD_MN; 1.
KW  Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
FT  METAL 26 26 MANGANESE (BY SIMILARITY).
FT  METAL 74 74 MANGANESE (BY SIMILARITY).
FT  METAL 159 159 MANGANESE (BY SIMILARITY).
FT  METAL 163 163 MANGANESE (BY SIMILARITY).
SQ  SEQUENCE 198 AA; 22209 MW; FB4F6B063198E5CC CRC64;

Query Match          53.3%; Score 615; DB 1; Length 198;
Best Local Similarity 56.6%; Pred. No. 9.4e-48;
Matches 112; Conservative 27; Mismatches 53; Indels 6; Gaps 2;

QY  26 KHTLPPLPAYDALEPSISKETMTLHTKHQTYVNGLNAAEESYSAAYGKEDVLTQVKL 85
DB  1 KHSPLDLPDYDGALEPHINAQIMQLHSHKHAAYVNNLVNTEKYQEALAKGDTVTAQIAL 60

QY  86 QSALKFNGGGCHNHSIFWKNLAPYGSSEATLSGPKLKAEESFGSFEAFKKFNADTAA 145
DB  61 QPALKFNGGGCHNHSIFWNLSPNGGGE---PKGELLEAIKRDGSGFEKFKLTAAVSG 117

QY  146 VQSGGWMGLNPLTKKLEVTITANQDPL---LTHPIIGVDIWEHAFYLYQKNVXPDYL 202
DB  118 VQSGGWMGLGNKRGKQQLQIAACPNQDPLQGTGTLPLIGIDVWEHAFYLYQKNVXPDYL 177

QY  203 AAVWSVINYKEAEARLQA 220
DB  178 KAIWNVINWENVTRYMA 195

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RESULT 10

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SODM_HYLLA          STANDARD;          PRT;          198 AA.
ID  SODM_HYLLA
AC  Q8HXP5;
DT  15-MAR-2004 (Rel. 43, Created)
DT  15-MAR-2004 (Rel. 43, Last sequence update)
DT  15-MAR-2004 (Rel. 43, Last annotation update)
DE  Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
GN  SOD2.
OS  Hylobates lar (Common gibbon).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX  NCBI_TaxID=9580;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=22271545; PubMed=12383507;
RA  Fukuhara R., Tezuka T., Kageyama T.;
RT  "Structure, molecular evolution, and gene expression of primate
RT  superoxide dismutases."
RL  Gene 296:99-109(2002).
CC  -!- FUNCTION: Destroys radicals which are normally produced within the
CC  cells and which are toxic to biological systems.
CC  -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC  -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC  -!- SUBUNIT: Homotetramer (By similarity).
CC  -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC  -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC  family.
-----
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EMBL; AB087276; BAC20355.1; ALT INIT.
InterPro; IPR001189; SODismutase.
Pfam; PF00081; sodfe; 1.
PRINTS; PR01703; MNSODISMATSE.
ProDom; PD000475; SODismutase; 1.
PROSITE; PS00088; SOD MN; 1.
Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
FT METAL 26 26 MANGANESE (BY SIMILARITY).
FT METAL 74 74 MANGANESE (BY SIMILARITY).
FT METAL 159 159 MANGANESE (BY SIMILARITY).
FT METAL 163 163 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 198 AA; 22234 MW; E266AFBBDB34566 CRC64;

Query Match          53.0%; Score 611; DB 1; Length 198;
Best Local Similarity 56.1%; Pred. No. 2.1e-47;
Matches 111; Conservative 27; Mismatches 54; Indels 6; Gaps 2;

QY 26 KHTLPPELAYDALEPSISKEITMLHTKHQTYVNGLNAAEESYSAAGVEDVLTQVKL 85
DB 1 KHSFLDPLDYGALEPHINAQIMQLHSHKHAAYVNNLVNTEEKYQALAKGDVTAQAL 60

QY 86 QSAKFNGGGGHINHSFLWKNLAPYGSBEATLSEGLPKAIEESFGSFEAFKKFNADTAA 145
DB 61 QPALKFNGGGGHINHSIFWTNLSPPNGGGE---PKGELLEAIKRDFFGSKFKELTATSVG 117

QY 146 VQSGGWMGLGNPLTKLEVTNTANQDPL---LTHPIIGVDIWEHAFYLYQKNVDPYL 202
DB 118 VQSGGWMGLGNPKERGHQIAACPNQDPLQGTGLIPLIGDIVEHAYLYQKNVDPYL 177

QY 203 AAVWSVINYKEAEARLQA 220
DB 178 KAIWNVINWENTERYMA 195

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RESULT 12

RESULT 11

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SODM_PANTR          STANDARD;          PRT;          198 AA.
ID  SODM_PANTR
AC  Q8HX7;
DT  15-MAR-2004 (Rel. 43, Created)
DT  15-MAR-2004 (Rel. 43, Last sequence update)
DT  15-MAR-2004 (Rel. 43, Last annotation update)
DE  Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
GN  SOD2.
OS  Pan troglodytes (Chimpanzee).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX  NCBI_TaxID=9598;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=22271545; PubMed=12383507;
RA  Fukuhara R., Tezuka T., Kageyama T.;
RT  "Structure, molecular evolution, and gene expression of primate
RT  superoxide dismutases."
RL  Gene 296:99-109(2002).
CC  -!- FUNCTION: Destroys radicals which are normally produced within the
CC  cells and which are toxic to biological systems.
CC  -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC  -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC  -!- SUBUNIT: Homotetramer (By similarity).
CC  -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC  -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC  family.
-----
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EMBL; AB087274; BAC20353.1; ALT INIT.
InterPro; IPR001189; SODismutase.
Pfam; PF00081; sodfe; 1.
PRINTS; PR01703; MNSODISMATSE.
ProDom; PD000475; SODismutase; 1.
PROSITE; PS00088; SOD MN; 1.
Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
FT METAL 26 26 MANGANESE (BY SIMILARITY).
FT METAL 74 74 MANGANESE (BY SIMILARITY).
FT METAL 159 159 MANGANESE (BY SIMILARITY).
FT METAL 163 163 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 198 AA; 22204 MW; F772EABBA6A9F4CD CRC64;

Query Match          52.9%; Score 610; DB 1; Length 198;
Best Local Similarity 56.1%; Pred. No. 2.6e-47;
Matches 111; Conservative 27; Mismatches 54; Indels 6; Gaps 2;

QY 26 KHTLPPELAYDALEPSISKEITMLHTKHQTYVNGLNAAEESYSAAGVEDVLTQVKL 85
DB 1 KHSFLDPLDYGALEPHINAQIMQLHSHKHAAYVNNLVNTEEKYQALAKGDVTAQAL 60

QY 86 QSAKFNGGGGHINHSFLWKNLAPYGSBEATLSEGLPKAIEESFGSFEAFKKFNADTAA 145
DB 61 QPALKFNGGGGHINHSIFWTNLSPPNGGGE---PKGELLEAIKRDFFGSKFKELTAAVSG 117

QY 146 VQSGGWMGLGNPLTKLEVTNTANQDPL---LTHPIIGVDIWEHAFYLYQKNVDPYL 202
DB 118 VQSGGWMGLGNPKERGHQIAACPNQDPLQGTGLIPLIGDIVEHAYLYQKNVDPYL 177

QY 203 AAVWSVINYKEAEARLQA 220
DB 178 KAIWNVINWENTERYMA 195

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SODM_PONPY STANDARD; PRT; 198 AA.

Q8HXP6;
 15-MAR-2004 (Rel. 43, Created)
 15-MAR-2004 (Rel. 43, Last sequence update)
 15-MAR-2004 (Rel. 43, Last annotation update)
 Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
 SOD2.
 Pongo pygmaeus (Orangutan).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 NCBI_TaxID=9600;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=22271545; PubMed=12383507;
 Fukuhara R., Tezuka T., Kageyama T.;
 "Structure, molecular evolution, and gene expression of primate
 superoxide dismutases.";
 Gene 296:99-109(2002).
 CC -!- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
 CC -!- SUBUNIT: Homotetramer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
 CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 CC family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AB087275; BAC20354.1; ALT INIT.
 CC InterPro: IPR001189; SODismutase.
 CC Pfam: PF00081; sodfe_1.
 CC Pfam: PF02777; sodfe_C_1.
 CC PRINTS: PR01703; MNSODISMUTASE.
 CC ProDom: PD000475; SODismutase; 1.
 CC PROSITE: PS00088; SOD MN; 1.
 CC Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
 KW METAL 26 26 MANGANESE (BY SIMILARITY).
 FT METAL 74 74 MANGANESE (BY SIMILARITY).
 FT METAL 159 159 MANGANESE (BY SIMILARITY).
 FT METAL 163 163 MANGANESE (BY SIMILARITY).
 SQ SEQUENCE 198 AA; 22204 MW; F772EABBA6A9F4CD CRC64;
 Query Match 52.9%; Score 610; DB 1; Length 198;
 Best Local Similarity 56.1%; Pred. No. 2.6e-47;
 Matches 111; Conservative 27; Mismatches 54; Indels 6; Gaps 2;
 QY 26 KHTLPPELAYDALEPSISKEIMTLHTKHQTVNGLNAAESYSAAVGKEDVLTQVKL 85
 Db 1 KHSLEPDPYDYGALPRHNAIQMLHSHKHAAYVNNLVNTEKYQALAKGVDVTAQIAL 60
 QY 86 QSALKFNGGGHINSLFWKLNAPYGSSEATLSBGLPKKAIIESFGSPFAFKKFNADTAA 145
 Db 61 QPALKFNGGGHINHSIPWNLSPNGGGE---PKGELLEAIKROFGSPDKFKELTAASVG 117
 QY 146 VQSGGWGLGNPLTKKLEVTNTANQDPL---LTHPIIGVDVWEHAFYLYQKVRKPDYL 202
 Db 118 VQSGGWGLGNPKRGRHGLQIAACPQDPLQGTGTLPLGLGVDWEHAYLYQKVRKPDYL 177
 QY 203 AAVWSVINYKEAEARLCA 220
 Db 178 KAIWNVINWENVTERYNA 195
 RESULT 13
 SODM_ARATH

ID AC SODM_ARATH STANDARD; PRT; 231 AA.

Q81235; Q9SRK3;
 16-OCT-2001 (Rel. 40, Created)
 18-FEB-2003 (Rel. 41, Last sequence update)
 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
 SODA OR MSDI OR AT3G10920 OR F9F8.26.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eustoids II; Brassicales; Brassicaceae; Arabidopsids.
 ON NCBI_TaxID=3702;
 [1]
 SEQUENCE FROM N.A.
 RP STRAIN=cv. Columbia;
 RC STRAIN=cv. Columbia;
 RX MEDLINE=98440686; PubMed=9765550;
 Kliebenstein D.J., Monde R.A., Last R.L.;
 "Superoxide dismutase in Arabidopsis: an eclectic enzyme family with
 RT disparate regulation and protein localization.";
 RL Plant Physiol. 118:637-650(1998).
 RN
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016720; PubMed=11130713;
 Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseld M.,
 RA Partmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
 RA Delsen M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
 De Simone V., Choisme N., Artiguenave F., Robert C., Brottier P.,
 RA Wincker P., Cattolico L., Weissbach J., Saurin W., Quetier F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
 RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
 RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
 RA Reichelt J., Schaefer M., Schoen O., Bargues M., Terol J., Clement J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
 RA Cooke R., Laudie M., Berger-Llauró C., Purnelle B., Masuy D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
 RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
 RA Mannhaupt G., Haase D., Schoof H., Rued S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
 RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
 RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
 RA Preuss D., Lin X., Niernan W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asanizu E.,
 RA Sasamoto S., Kimura T., Ideawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
 "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 408:820-822(2000).
 [3]
 SEQUENCE FROM N.A.
 RP STRAIN=cv. Columbia;
 RX MEDLINE=22954850; PubMed=14593172;
 Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
 RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
 RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
 Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
 Arakawa T., Bann J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
 RA Chao Q., Choy N., Enju N., Goldsmith A.D., Gurjal M., Hansen N.F.,
 RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
 RA Khan S., Koesena E., Ishida J., Jiang P.X., Jones T., Kawai J.,
 RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
 RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
 RA Yuan S., Shinozaki K., Davis R., Theologis A., Ecker J.R.;
 "Empirical analysis of transcriptional activity in the Arabidopsis
 RT genome.";
 RL Science 302:842-846(2003).
 CC -!- FUNCTION: Destroys radicals which are normally produced within the

```

CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC -----
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CC -----
CC EMBL; AF061518; AAC24832.1; -
CC EMBL; AC009991; AAF01529.1; -
CC EMBL; AY072495; AAL66910.1; -
CC EMBL; AY059807; AAL24289.1; -
CC PIR; T50827; T50827.
CC HSRP; P04179; IABM.
CC InterPro: IPR001189; SODismutase.
CC Pfam; PF00081; sodfe, 1.
CC Pfam; PF02777; sodfe C; 1.
CC PRINTS; PR01703; MNSODISMUTASE.
CC ProDom; PD000475; SODismutase; 1.
CC PROSITE; PS00088; SOD_MN; 1.
CC Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
KW Transit peptide.
KW TRANSIT 1 29 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 30 231 SUPEROXIDE DISMUTASE [MN].
FT METAL 59 59 MANGANESE (BY SIMILARITY).
FT METAL 103 103 MANGANESE (BY SIMILARITY).
FT METAL 192 192 MANGANESE (BY SIMILARITY).
FT METAL 196 196 MANGANESE (BY SIMILARITY).
FT METAL 169 169 V -> F (IN REF. 1).
FT CONFLICT 169 169
SQ SEQUENCE 231 AA; 25444 MW; 2DBD5560A9E8AD7D CRC64;

Query Match 52.6%; Score 606; DB 1; Length 231;
Best Local Similarity 60.2%; Pred. No. 7.2e-47;
Matches 115; Conservative 21; Mismatches 51; Indels 4; Gaps 1;

Qy 28 TLPELPAYDALEPSISKEIMTLHTKHQTYVNGLNAAEESYSAAGKEDVLTQVKLQS 87
Db 32 TLPDLPDYGALEPAISGEIMQIHQKHQYVTVNNALQQLQAVNKGDASTVVKLQS 91

Qy 88 ALKENGGGHINSLFWKNLAPYGSBEATLSEGLKKAIEESFGSFEAFKKFNADTAQV 147
Db 92 AIKENGGGHVNHSIFWKNLAPSESGGGGPPKGLSGLSAIDAHFGLGLVKMSAEGAAVQ 151

Qy 148 GSGGWLGLNPLTKKLEVTITANODPLTH---IPIIGVDIWEHAFYLYQKNVKKPDYLA 203
Db 152 GSGVNLGLDKELKLVVDITANODPLTVTKGSLVPLVGLVDIWEHAFYLYQKNVRPEYLK 211

Qy 204 AVWSVINYKEA 214
Db 212 NVWKVINWKYA 222

RESULT 14
SODM_CALJA STANDARD; PRT; 198 AA.
AC QBHXPO;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
GN SOD2.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC Callithrix.

```

```

OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22271545; PubMed=12383507;
RA Fukuhara R., Tezuka T., Kageyama T.;
RT "Structure, molecular evolution, and gene expression of primate
RT superoxide dismutases.";
RL Gene 296:99-109(2002).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB087281; BAC20360.1; ALT_INIT.
CC InterPro: IPR001189; SODismutase.
CC Pfam; PF00081; sodfe, 1.
CC Pfam; PF02777; sodfe C; 1.
CC PRINTS; PR01703; MNSODISMUTASE.
CC ProDom; PD000475; SODismutase; 1.
CC PROSITE; PS00088; SOD_MN; 1.
CC Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
FT METAL 26 26 MANGANESE (BY SIMILARITY).
FT METAL 74 74 MANGANESE (BY SIMILARITY).
FT METAL 159 159 MANGANESE (BY SIMILARITY).
FT METAL 163 163 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 198 AA; 22248 MW; E7F8960B8C56F2CA CRC64;

Query Match 52.5%; Score 605; DB 1; Length 198;
Best Local Similarity 55.6%; Pred. No. 7.3e-47;
Matches 110; Conservative 28; Mismatches 54; Indels 6; Gaps 2;

Qy 26 KHTPELPAYDALEPSISKEIMTLHTKHQTYVNGLNAAEESYSAAGKEDVLTQVKL 85
Db 1 KHSPLDLPDYGALEPHINAIQMLHSHKHAAYVNNLNDTEKYKEALAKGDVTAQIAL 60

Qy 86 QSALKFNGGGHINSLFWKNLAPYGSBEATLSEGLKKAIEESFGSFEAFKKFNADTAA 145
Db 61 QPALKFNGGGHINHSIFWNLSPNGGGE---PKGELLEAIKRDGFSDFKFKERLTAAAVG 117

Qy 146 VQSGGWLGLNPLTKKLEVTITANODPL---LTHPIIGVDIWEHAFYLYQKNVKKPDYL 202
Db 118 VQSGGWLGLNPKERGHQLQAACPNQDPLQGTGLIPLGLDIDWEHAFYLYQKNVRPDL 177

Qy 203 AAVWSVINYKEAEARLQA 220
Db 178 KAIWNVINWENVTERYWA 195

RESULT 15
SODM_CEBAP STANDARD; PRT; 198 AA.
AC QBHXPL;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
GN SOD2.
OS Cebus apella (Brown-capped capuchin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus.
OX NCBI_TaxID=9515;

```

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22271545; PubMed=12383507;
RA Fukuhara R., Tezuka T., Kageyama T.;
RT "Structure, molecular evolution, and gene expression of primate
RT superoxide dismutases.";
RL Gene 296:99-109(2002).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB087280; BAC20359.1; ALT INIT.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR Pfam; PF02777; sodfe_C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
FT METAL 26 26 MANGANESE (BY SIMILARITY).
FT METAL 74 74 MANGANESE (BY SIMILARITY).
FT METAL 159 159 MANGANESE (BY SIMILARITY).
FT METAL 163 163 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 198 AA; 22248 MW; E7F8860B8C56F2CA CRC64;

Query Match 52.5%; Score 605; DB 1; Length 198;
Best Local Similarity 55.6%; Pred. No. 7.3e-47;
Matches 110; Conservative 28; Mismatches 54; Indels 6; Gaps 2;

QY 26 KHTLPPLPYDALEPSISKEIMTLHHTKHQTYVNGLNAAESYSAAYGKEDVLTQVKL 85
Db 1 KHSPLDLPYDYGALPHINAQIMQLHSHKHAAYVNNLNDTEKYKEALAKGDVTAQIAL 60

QY 86 QSALKFNGGGHINHSFWKNLAPYSEBEATLSEGPLKKAIEBSFGSPFAFKKFNADTAA 145
Db 61 QPALKFNCGGGINHSIFWTNLSPNGGGE---PKGELLEAIKRFDFGSKFKERLTAASVG 117

QY 146 VOGSGWGLGLNPLTKKLVTTTANQDPL---LTHPIIGVDIWEHAFYLYQKNVYPDYL 202
Db 118 VOGSGWGLGFNKRGHGLQIACFNQDPLQGTTLGLIPLIGDVMWEHAYLYQKNVYPDYL 177

QY 203 AAVWSVINYKEAEARLQA 220
Db 178 KAINVINWENTERYWA 195
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Search completed: March 30, 2004, 17:14:38
Job time : 19 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2004, 17:09:18 ; Search time 26 seconds
(without alignments)
821.328 Million cell updates/sec

Title: US-09-727-855b-5

Perfect score: 1153

Sequence: 1 MSVRASLSVSRSQTTFVAPAA.....AAVWSVINYKEARLQAAL 222

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	634.5	55.0	222	1 DSRPN	superoxide dismuta
2	634.5	55.0	222	2 I57023	superoxide dismuta
3	629.5	54.6	222	1 I51918	superoxide dismuta
4	620	53.8	222	1 DSHUN	superoxide dismuta
5	614	53.3	231	2 T08181	superoxide dismuta
6	612.5	53.1	237	2 T50830	superoxide dismuta
7	601	52.1	231	2 T50827	superoxide dismuta
8	600	52.0	204	2 S65795	superoxide dismuta
9	600	52.0	228	2 T50828	superoxide dismuta
10	600	52.0	240	1 DSPMN	superoxide dismuta
11	596	51.7	233	2 T06258	superoxide dismuta
12	595	51.6	233	2 S39492	superoxide dismuta
13	592	51.3	228	2 S03639	superoxide dismuta
14	590.5	51.2	231	2 T04072	probable superoxid
15	590.5	51.2	231	2 T04312	probable superoxid
16	590.5	51.2	233	2 B48684	superoxide dismuta
17	590	51.2	233	2 T06801	probable superoxid
18	587	50.9	231	2 T06801	probable superoxid
19	584.5	50.7	221	2 JC5122	superoxide dismuta
20	584	50.7	235	2 S03839	superoxide dismuta
21	582	50.5	228	2 T08045	superoxide dismuta
22	581	50.4	205	2 T50829	superoxide dismuta
23	574	49.8	240	2 T50831	superoxide dismuta
24	574	49.8	241	2 T47752	superoxide dismuta
25	572	49.6	218	2 S52721	superoxide dismuta
26	570.5	49.5	232	2 C48684	superoxide dismuta
27	560	48.6	218	2 T50070	superoxide dismuta
28	558	48.4	233	2 A48684	superoxide dismuta
29	553	48.0	198	2 T09799	superoxide dismuta

30	548	47.5	187	2 T50832	superoxide dismuta
31	543.5	47.1	233	2 T09788	probable superoxid
32	535.5	46.4	207	2 A81688	superoxide dismuta
33	529.5	45.9	206	2 H71531	superoxide dismuta
34	514.5	44.6	207	2 B86498	superoxide dismuta
35	514.5	44.6	207	2 B72124	superoxide dismuta
36	504.5	43.8	226	2 B69709	superoxide dismuta
37	496	43.0	204	2 S22053	superoxide dismuta
38	495	42.9	204	1 DSBNSF	superoxide dismuta
39	492	42.7	202	2 JC1272	superoxide dismuta
40	492	42.7	202	2 AG1254	superoxide dismuta
41	491.5	42.6	196	2 A39223	superoxide dismuta
42	491.5	42.6	223	2 S48831	superoxide dismuta
43	491.5	42.6	223	2 S48832	superoxide dismuta
44	488	42.3	202	2 S20019	superoxide dismuta
45	488	42.3	202	2 AE1617	superoxide dismuta

ALIGNMENTS

RESULT 1

DSRN

superoxide dismutase (EC 1.15.1.1) (Mn) precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 11-Jun-1999

C:Accession: S21661, S06310

R;Ho, Y.S.; Howard, A.J.; Crapo, J.D.

submitted to the EMBL Data Library, October 1990

A:Reference number: S21661

A:Accession: S21661

A:Molecule type: DNA

A:Residues: 1-222 <HOY1>

A:Cross-references: EMBL:X56600; NID:g57272; PIDN:CAA39937.1; PID:g57273

R;Ho, Y.S.; Crapo, J.D.

Nucleic Acids Res. 15, 10070, 1987

A:Title: Nucleotide sequences of cDNAs coding for rat manganese-containing superoxide dis

A:Reference number: S06310; MUID:88096516; PMID:3697077

A:Accession: S06310

A:Molecule type: mRNA

A:Residues: 1-166,'H',168-222 <HOY2>

A:Cross-references: EMBL:X00497; NID:g56690; PIDN:CAA68549.1; PID:g56691

A:Note: 167-Gln was also found

C:Genetics:

A:Gene: SOD2

A:Introns: 8/2; 76/1; 115/1; 175/1

C:Function:

A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen

C:Superfamily: superoxide dismutase (Mn)

C:Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase

F:1-24/Domain: transit peptide (mitochondrion) #status predicted <TNP>

F:25-222/Product: superoxide dismutase (Mn) #status predicted <MNT>

F:50,98,183,187/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 55.0%; Score 634.5; DB 1; Length 222;

Best Local Similarity 55.4%; Pred. No. 6.5e-49;

Matches 123; Conservative 30; Mismatches 58; Indels 11; Gaps 4;

QY 1 MSVRASLSVSRSQTTFVAPAFQI--RAKHTLPDPVAYDALEPSISKBIITLHHTKHQT 58

Db 1 MLCRAACSAGRR---LGPAASTAGSRHKSFLPDPYDYGALPHINAQIMQLHSHKHAT 57

QY 59 YNGLNAAESVSAAGKEDVLTQVKLSALPENGCGGHINHSIFWNLAAPYSGEATLSE 118

Db 58 YNNLNVTTEKHYHEALAKGDVTTQVALQPALPENGCGGHINHSIFWNLSFKGGGE---PK 114

QY 119 GPLKKAIESFGSFEAFKKFNADTAAGVSGSGWGLGNPLTKKLEVTITANODPL---L 175

Db 115 GELLEIAIKDDFGSFEKFKELTAVSVGVSGSGWGLGFNKEQGRLOIAACSNODPLQGT 174

QY 176 THPIIFGVDIWEHAFYLYQYKNKVPDYLAAVWSVINYKEABAR 217

Db 175 GLIPLIGIDWEHAYLYQYKNRDPYLKAIWNVINWENVSQR 216

```
151918
superoxide dismutase (EC 1.15.1.1) (Mn) precursor - mouse
C:Species: Bos primigenius taurus (cattle)
C>Date: 15-Oct-1996 #sequence_revision 15-Aug-1997 #text_change 21-Jul-2000
C:Accession: I51918; I64848; I64850
R:Meyrick, B.; Magnuson, M.A.
A:Title: Identification and functional characterization of the bovine manganous superoxide
dismutase
A:Reference number: 151918; MUID:94121934; PMID:8292376
A:Accession: I51918
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-222 <MEY1>
A:Cross-references: GB:L22092; NID:G498259; PIDN:AAA30655.1; PID:G498260
A:Accession: I64848
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7 <PRA2>
A:Cross-references: GB:L22093; NID:G498261; PIDN:AAA30656.1; PID:G552330
A:Accession: I64850
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7, 'R' <MEY3>
A:Cross-references: GB:S67819; NID:G460572; PIDN:AAD14001.1; PID:G4261701
C:Genetics:
A:Gene: MnSOD
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
F:1-24/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:25-222/Product: superoxide dismutase (Mn) #status predicted <MAT>
F:50,98,183,187/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 54.6%; Score 629.5; DB 2; Length 222;
Best Local Similarity 54.3%; Pred. No. 1.8e-48;
Matches 121; Conservative 32; Mismatches 63; Indels 7; Gaps 3;

Qy 1 MSVRASLSVSROTFVAPAAQIRAKHTLPPEYDALPEISKEIMTLHHTKHQTYV 60
Db 1 MLSPAACT-SRRLVPALSVLGSQKSLPDLFDYDGALEPHINAQIMQLHSHKHAAYV 59

Qy 61 NGLNAEESYSAAVGKEDVLTQVKLSALKPFGGHHNHSIFWNLAPYGSSEATLSEGP 120
Db 60 NNLNAEKEYHEALAKGDTVTAQALQALPALKFNGGHHNHSIFWNLSPNGGGE---PKGE 116

Qy 121 LKKAIESFGSFEAFKKFNADTAAGVSGSGWGLNPLTKLEVTITANODPL---LTH 177
Db 117 LLEAIKRDGFSFAKFEKLTAVSVGVSGSGWGLNPLTKLEVTITANODPL---LTH 176

Qy 178 IPIIGVDIWEHAFYLYQKNVPDYLAADVSVINYKEAEARLQA 220
Db 177 IPLLGDVWEHAYLYQKNVPDYLAADVSVINYKEAEARLQA 219

RESULT 4
DSHUN
superoxide dismutase (EC 1.15.1.1) (Mn) precursor [validated] - human
C:Species: Homo sapiens (man)
C>Date: 04-Dec-1986 #sequence_revision 06-Feb-1995 #text_change 20-Apr-2000
C:Accession: S13162; S02272; S11756; S00356; S02230; S00663; A92447; I38033; A00520; A277;
R:Church, S.L.
A:Title: Manganese superoxide dismutase: nucleotide and deduced amino acid sequence of a
A:Reference number: S13162; MUID:91027939; PMID:1699607
A:Accession: S13162
A:Molecule type: mRNA
A:Residues: 1-222 <CHU>
A:Note: cross-reference GB:M34665 cited in paper is not correct
R:Wise, J.R.; Clark, J.C.; Burhans, M.S.; Kropp, K.E.; Korfhagen, T.R.; Whitsett, J.A.
Biochim. Biophys. Acta 994, 30-36, 1989
A:Title: Synthesis and processing of the precursor for human manganous superoxide dismutase
A:Reference number: S02272; MUID:89076921; PMID:2462451
```

```
157023
superoxide dismutase (EC 1.15.1.1) (Mn) precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Jun-1999
C:Accession: I57023; JC4047; S36129; A25581
R:DiSilvestre, D.; Kleeberger, S.R.; Johns, J.; Levitt, R.C.
Mamm. Genome 6, 281-284, 1995
A:Title: Structure and DNA sequence of the mouse MnSOD gene.
A:Reference number: I57023; MUID:95337589; PMID:7613035
A:Accession: I57023
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-222 <RES>
A:Cross-references: GB:S78846; NID:G1037119; PIDN:AAB34899.1; PID:G1037120
R:Jones, P.L.; Kucera, G.; Gordon, H.; Boss, J.M.
Gene 153, 155-161, 1995
A:Title: Cloning and characterization of the murine manganous superoxide dismutase-encod
A:Reference number: JC4047; MUID:95180711; PMID:7875582
A:Accession: JC4047
A:Molecule type: DNA
A:Residues: 1-137, 'M', 139-222 <JON>
A:Cross-references: GB:I35525
R:Sun, Y.
submitted to the EMBL Data Library, November 1992
A:Reference number: S36129
A:Accession: S36129
A:Molecule type: mRNA
A:Residues: 1-222 <SUN>
A:Cross-references: EMBL:Z18857; NID:G288504; PIDN:CAA79308.1; PID:G288505
R:Hallewell, R.A.; Mullenbach, G.T.; Stempien, M.M.; Bell, G.I.
Nucleic Acids Res. 14, 9539, 1986
A:Title: Sequence of a cDNA coding for mouse manganese superoxide dismutase.
A:Reference number: A25581; MUID:87091590; PMID:3797253
A:Accession: A25581
A:Molecule type: mRNA
A:Residues: 1-17, 'V', 19-137, 'M', 139-222 <HAL>
A:Cross-references: GB:X04972; NID:G53449; PIDN:CAA28645.1; PID:G53450
C:Genetics:
A:Gene: Sod-2
A:Introns: 8/2; 76/1; 115/1; 175/1
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
F:1-24/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:25-222/Product: superoxide dismutase (Mn) #status predicted <MAT>
F:50,98,183,187/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 55.0%; Score 634.5; DB 2; Length 222;
Best Local Similarity 55.6%; Pred. No. 6.5e-49;
Matches 124; Conservative 30; Mismatches 62; Indels 7; Gaps 3;

Qy 1 MSVRASLSVSROTFVAPAAQIRAKHTLPPEYDALPEISKEIMTLHHTKHQTYV 60
Db 1 MLCRAACSTGRRLGVPAGAAGS-RHKHSPLDLPDYDGALEPHINAQIMQLHSHKHAAYV 59

Qy 61 NGLNAEESYSAAVGKEDVLTQVKLSALKPFGGHHNHSIFWNLAPYGSSEATLSEGP 120
Db 60 NNLNAEKEYHEALAKGDTVTAQALQALPALKFNGGHHNHSIFWNLSPKGGGE---PKGE 116

Qy 121 LKKAIESFGSFEAFKKFNADTAAGVSGSGWGLNPLTKLEVTITANODPL---LTH 177
Db 117 LLEAIKRDGFSFAKFEKLTAVSVGVSGSGWGLNPLTKLEVTITANODPL---LTH 176

Qy 178 IPIIGVDIWEHAFYLYQKNVPDYLAADVSVINYKEAEARLQA 220
Db 177 IPLLGDVWEHAYLYQKNVPDYLAADVSVINYKEAEARLQA 219

RESULT 3
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C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
F;1-24/Domain: transit peptide (mitochondrion) #status predicted <NP>
F;25-222/Product: superoxide dismutase (Mn) #status experimental <MAT>
F;50,98,183,187/Binding site: manganese (His, His, Asp, His) #status experimental

Query Match 53.8%; Score 620; DB 1; Length 222;
Best Local Similarity 53.6%; Pred. No. 1.3e-47;
Matches 118; Conservative 31; Mismatches 61; Indels 10; Gaps 4;

QY 6 SLGSVSQTFFVAPAAFOI--RAKHTLPPEAYDALEPSISKEIMTLHHTKHQTYYNGL 63
DB :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | |
 5 AVCGTSRQ--LAPALGVLSGRQSRLPDPDYDGALEPHINAQMQLHSKHAAVVNVL 62

QY 64 NAAEESYAAGVEDVTQVKLOSAIKFNCGGHINHSFWKNLA PYSGSEATLSEGPLKK 123
DB :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | |
 63 NVTEEKYEALAKGDVTAQIALPALKFNGGGHINHSLFTNLSPNGGGE---PKGELLE 119

QY 124 AIESFGSFEAFKKFKFNADTAAVGSGWGWLGNLTPTTKLEVTTITANQPDL---LTHPI 180
DB :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | |
 120 AIKRDFSGFDKFEKLTAASVGVQGSGWGLGFNKRGHLQAACPNQDPLQGTGTLPL 179

QY 181 IGVDWEHAFLYOYNKVXPDYLAAVWSVINVEAEARLQA 220
DB :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | |
 180 LGIDVWEHAYLYQNVRPYDKAIWNVINWENVIERYMA 219

RESULT 5
T08181
superoxide dismutase (EC 1.15.1.1) (Mn) - radish
C;Species: Raphanus sativus (radish)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Apr-2000
C;Accession: T08181
R;Kwon, S.I.; An, C.S.
submitted to the EMBL Data Library, April 1998
A;Reference number: Z16401
A;Accession: T08181
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-231 <KW0>
A;Cross-references: EMBL:AF061333; NID:g3108344; PID:g3108345
C;Genetics:
A;Gene: sod
C;Function:
A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; oxidoreductase
F;55,103,192,196/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 53.3%; Score 614; DB 2; Length 231;
Best Local Similarity 57.5%; Pred. No. 4.6e-47;
Matches 122; Conservative 20; Mismatches 54; Indels 16; Gaps 2;

QY 7 LSSYSRQTFVAPAFAOIPRAKHTLPPELAYDALEPSISKEIMTLHHTKHQTYYNGNA 66
DB :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | |
 23 LGSSIOTF-----TLPDLPDYSALEPAISGEIMOQHQQHQAVTYNNYA 70

QY 67 EEYSYAAGVEDLVLTQVKLOSAIKFNCGGHINHSFWKNLA PYSGSEATLSEGPKKAIE 126
DB :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | |
 71 LEQLDAQNVKGDSAAVVKLSAQIAKFNCGSHVNHSIFWKNLAPVKEGGPGPKGSLGAID 130

QY 127 ESFGSFEAFKKFKFNADTAAVGSGWGWLGNLTPTTKLEVTTITANQDLLTH----TPILG 182
DB :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | |
 131 TSFGGLEGLVKKMSAEGAAGVQSGMWLGLDRELKXLVDDTTANQDPLTVTKGSSLVELVG 190

QY 183 VDIWEHAPLYOKNVKP DYLLAAVWSVINVEA 214
DB :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | |
 191 IDVWEHAYLYQNVRPYDKLNWVKVINWXYA 222

RESULT 6
T50830
superoxide dismutase (EC 1.15.1.1) (Mn) precursor, mitochondrial [similarity] - leafy sp.

[illegible]

A;Residues: 1-231 <WUG>
A;Cross-references: EMBL:U72212; NID:g1622928; PIDN:AAB68035.1; PID:g1621627
C;Genetics:
A;Gene: SOD3.1
A;Genome: nuclear
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
F;55,103,192,196/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 51.7%; Score 596; DB 2; Length 231;
Best Local Similarity 55.2%; Pred. No. 1.8e-45;
Matches 116; Conservative 23; Mismatches 65; Indels 6; Gaps 2;

QY 18 PAFAQTAKHTLPPLPAYDALEPSISKETIMLTHTKHQTYVNGLNAAEESYSAAVGKE 77
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 22 PAAARGVATFTLPDPFYDYGALPAVSGEIMRLHFHKHATYVANYNKALEQLDAAVSKG 81
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 78 DVLTVQLQSALKFNGGGGHINHSFWKNLAPYGSSEATLSEGLPKKAIESFGSFSAFFKK 137
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 82 DASAVHLQGAIKFNKGSGGVNHISFWKNLKPISGEGGEAPHGKLGWAIEDFSIEKLIK 141
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 138 KFNADTAAVQSGWGWLGNLPTTKKLEYTTTANQDPLLT-----HIPIIGVDIWEHAFYL 192
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 142 KMAEGAALQGSGVWLALDKAEKLSVETIPNQDPLVTKGSNLH-PLLGDVWEHAYYL 200
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 193 QYKNVKPDYLAADVMSVINYNKAEARLQAAL 222
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 201 QYKNVRPDYLTNIWKVNWNKYAGEYEKVL 230
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

RESULT 12
S39492
superoxide dismutase (EC 1.15.1.1) (Mn) - Para rubber tree
C;Species: Hevea brasiliensis (Para rubber tree)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 28-May-1999
C;Accession: S39492
R;Miao, Z.; Gaynor, J.J.
Plant Mol. Biol. 23, 267-277, 1993
A;Title: Molecular cloning, characterization and expression of Mn-superoxide dismutase f
A;Reference number: S39492; MUID:94033306; PMID:8219064
A;Accession: S39492
A>Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <MTA>
A;Cross-references: GB:I11707; NID:g348136; PIDN:AAA16792.1; PID:g348137
C;Function:
A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen a
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; oxidoreductase
F;55,103,192,196/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 51.6%; Score 595; DB 2; Length 233;
Best Local Similarity 53.3%; Pred. No. 2.2e-45;
Matches 121; Conservative 30; Mismatches 58; Indels 18; Gaps 5;

QY 1 MSVRASLSSVSRQTFVAPAAF-----QIRAKHT--LPPEPYADALEPSPISKEIMTLH 51
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 1 MALR---SLVTRKNL--PSAFKAATGLGRLGTFTSLPDLPYDYGALEPAISGEIMQLH 55
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 52 HTKHHQTYVNGLNAAEESYSAAVGEDVLTQVQLSALKFNGGGGHINHSIFWKNLAPVGS 111
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 56 HQKHQTYITTNKALEQNDAIEKSDSAVVKLQSAIRFNGGGGVNHNSIFWKNLAPVRE 115
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 112 EEATLSEGLPKKAIESFGSFSAFFKKFNADTAADVQSGWGWLGLNPLTKKLEVTTTANQ 171
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 116 GGGELPHGSLGWADADPGSLBKLQLMNAEGALQSGGWWLADOKELKKLVETTANQ 175
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 172 DPLLTTH----IPIIGVDIWEHAFYIQYKNVKPDYLAADVMSVINYKEA 214
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 176 DPLVTKGTLVLLGIDVWEHAYYIQYKNVRPDYLNKINWKVMWKYA 222
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

RESULT 13

